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OM protein - protein search, using sw model

Run on: August 4, 2005, 15:22:33 ; Search time 165 Seconds
(without alignments)
274.248 Million cell updates/sec

Title: US-09-897-438B-2
Perfect score: 625
Sequence: 1 ECGGTHMGNAVTFCEPYGP.....FQWKDPSLRVGEYKCMAL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	117	5	AB806244
2	625	100.0	589	5	AAE13606
3	625	100.0	3461	5	AB805008
4	625	100.0	3461	5	AB857065
5	625	100.0	3461	7	AD860142
6	572	91.5	3427	7	ADJ69818
7	572	91.5	3460	5	AB805007
8	572	91.5	3460	7	AD860143
9	572	91.5	3460	7	ADN95182
10	572	91.5	3460	8	ADQ20919
11	572	91.5	3460	8	ADQ88204
12	572	91.5	3470	4	ABG25297
13	499	79.8	432	5	AAE13605
14	499	79.8	623	5	AAE13607
15	224	35.8	84	8	ABO56700
16	190	30.4	70	4	ABG55221
17	107	17.1	28	4	AAW74141
18	107	17.1	28	4	AAW61384
19	107	17.1	28	5	ABG55918
20	107	17.1	28	5	ABG44060
21	83	13.3	639	1	AAE40212
22	81.5	13.0	468	4	ABG25295
23	81	13.0	616	2	AAW55976
24	81	13.0	616	2	AAW55976
25	81	13.0	616	2	AAW55980

26	81	13.0	616	2	AAW55979	AAW55979	Aspergill
27	81	13.0	616	3	AAE15181	AAE15181	Aspergill
28	81	13.0	616	3	AAE15176	AAE15176	Aspergill
29	81	13.0	616	3	AAE15178	AAE15178	Aspergill
30	81	13.0	616	3	AAE15184	AAE15184	Aspergill
31	81	13.0	616	3	AAE15180	AAE15180	Aspergill
32	81	13.0	616	3	AAE15179	AAE15179	Aspergill
33	81	13.0	621	2	AAW55978	AAW55978	Aspergill
34	81	13.0	621	3	AAE15182	AAE15182	Aspergill
35	81	13.0	621	3	AAE15183	AAE15183	Aspergill
36	81	13.0	630	1	AAE81876	AAE81876	Sequence
37	81	13.0	640	4	AAE17741	AAE17741	A. niger
38	81	13.0	640	4	AAE161905	AAE161905	A. niger
39	74.5	11.9	834	4	ABG25296	ABG25296	Novel hum
40	73	11.7	1095	6	ABP96630	ABP96630	Alpha-amyl
41	71.5	11.4	91	8	ABO55728	ABO55728	Human gen
42	70.5	11.3	271	5	ABE29970	ABE29970	Streptoco
43	70.5	11.3	279	5	ABP25985	ABP25985	Streptoco
44	69.5	11.1	667	4	ABE70456	ABE70456	Drosophi
45	68.5	11.0	326	7	ADH70051	ADH70051	C. neofor
46	68.5	11.0	572	8	ADJ50225	ADJ50225	Oil-asso
47	68.5	11.0	611	8	ADJ49056	ADJ49056	Oil-asso
48	68.5	11.0	611	8	ADJ59749	ADJ59749	B. subtil
49	68	10.9	426	6	ABP96582	ABP96582	Cow IgE h
50	68	10.9	459	3	AAE20638	AAE20638	Arabidops
51	68	10.9	461	3	AAE20637	AAE20637	Arabidops
52	68	10.9	462	8	ADK47072	ADK47072	Streptoco
53	68	10.9	472	6	ABU02501	ABU02501	S. pneumo
54	68	10.9	473	8	ADR94638	ADR94638	Novel S.
55	68	10.9	512	3	AAE20636	AAE20636	Arabidops
56	68	10.9	553	7	ADP17839	ADP17839	Chimeric
57	68	10.9	574	7	ADBE4863	ADBE4863	Human pro
58	67.5	10.8	3623	2	AAE27020	AAE27020	Rat cubil
59	67	10.7	90	3	AAE10197	AAE10197	Arabidops
60	67	10.7	110	3	AAE15092	AAE15092	Arabidops
61	67	10.7	222	5	AAE91372	AAE91372	Human sec
62	67	10.7	222	5	ABG65027	ABG65027	Human alb
63	67	10.7	222	8	ADL78294	ADL78294	Albunin f
64	67	10.7	225	6	ABR41331	ABR41331	Human DIT
65	67	10.7	267	5	AAE91349	AAE91349	Human sec
66	67	10.7	267	5	ABG65030	ABG65030	Human alb
67	67	10.7	267	8	ADL78297	ADL78297	Albunin f
68	67	10.7	339	4	AAU09964	AAU09964	Human cyt
69	67	10.7	356	7	ABO65401	ABO65401	Klebsiell
70	67	10.7	489	5	AAE91371	AAE91371	Human sec
71	67	10.7	489	5	ABG65029	ABG65029	Human alb
72	67	10.7	489	8	ADL78296	ADL78296	Albunin f
73	67	10.7	514	5	AAE48334	AAE48334	Human spe
74	67	10.7	528	5	AAE91399	AAE91399	Human sec
75	67	10.7	743	7	ADG87098	ADG87098	Glucocamyl
76	66.5	10.6	89	2	AAE137665	AAE137665	Amino acyl
77	66.5	10.6	544	6	ABU25791	ABU25791	Protein e
78	66	10.6	624	4	AAE48170	AAE48170	Thermoaac
79	66	10.6	743	7	ADG87094	ADG87094	Glucocamyl
80	66	10.6	1098	2	AAE93932	AAE93932	Haemophil
81	66	10.6	1524	4	ABG25288	ABG25288	Novel hum
82	65.5	10.5	53	4	AAE41552	AAE41552	Propionib
83	65.5	10.5	126	4	ABM38041	ABM38041	Propionib
84	65.5	10.5	153	6	AAE78909	AAE78909	C. glutam
85	65.5	10.5	209	3	AAE51026	AAE51026	Arabidops
86	65.5	10.5	234	8	ADG86177	ADG86177	Aspergill
87	65.5	10.5	269	4	ABE69533	ABE69533	Drosophi
88	65.5	10.5	372	8	ADG23806	ADG23806	Bacteri
89	65.5	10.5	374	3	AAE41650	AAE41650	Arabidops
90	65.5	10.5	465	6	ABJ25380	ABJ25380	Aspergill
91	65.5	10.5	549	6	AAE30782	AAE30782	C. glutam
92	65.5	10.5	549	8	ADG47934	ADG47934	Beta-vulg
93	65.5	10.5	564	3	AAE41649	AAE41649	Arabidops
94	65.5	10.5	577	3	AAE41648	AAE41648	Arabidops
95	65.5	10.5	611	8	ADJ50073	ADJ50073	Oil-asso
96	65.5	10.5	620	7	ADW47277	ADW47277	Protocodac
97	65.5	10.5	624	6	ABJ25980	ABJ25980	Aspergill
98	65.5	10.5	941	5	ABE93761	ABE93761	Herbicida

99 65.5 10.5 1042 4 ABB60137
100 65.5 10.5 1102 4 ABB62029

Abb60137 Drosophila
Abb62029 Drosophila

ALIGNMENTS

RESULT 1

ABB06244
ID ABB06244 standard; protein; 117 AA.

XX ABB06244;

AC 21-MAY-2002 (first entry)

DE Mouse reelin protein CR-50 epitope region protein SEQ ID NO:2.

KW Mouse; reelin protein CR-50 epitope region; elucidation; neuron;
cerebral disturbance; reelin protein; neuroprotective.

XX Mus musculus.

PN JP2002017361-A.

PD 22-JAN-2002.

PF 04-JUL-2000; 2000JP-00202801.

PR 04-JUL-2000; 2000JP-00202801.

PA (RIKE) RIKEN KK.

DR WPI; 2002-221707/28.

XX N-PSDB; ABL40165.

PT Reelin protein CR-50 epitope region, useful for diagnosis and treatment
of cerebral disturbance.

PS Claim 3; Page 11-12; 16pp; Japanese.

XX The present sequence represents the mouse reelin protein CR-50 epitope
region, which contains the CR-50 antibody recognition site and is free
from F-spondin domains and repetitive sites. Also described are: (1) an
expression vector comprising a polynucleotide encoding a reelin protein
epitope region; (2) host cells with transfected the expression vector;
(3) polypeptides prepared by culture of the host cells; and (4)
polynucleotides comprising the 351 base sequence given in ABL40165 which
encodes the 117 amino acid sequence given in ABB06244; and (5) use of the
polynucleotide for diagnosis and/or treatment of diseases caused by
abnormal positioning of neural cells, and stimulation of association of
neuroprotective activity, and can be used in the diagnosis and treatment
of cerebral disturbance due to an abnormal reelin gene and positioning of
neurons

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 625; DB 5; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-64;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EOCGTIMGNNAVTFCEPYGPRLTTTCINTTASVLOFSIGSGCRFSYSDPSITVSAAK 60

DB 1 EOCGTIMGNNAVTFCEPYGPRLTTTCINTTASVLOFSIGSGCRFSYSDPSITVSAAK 60

QY 61 NNTAWIOLKIRAPSNVSTVTHILYLPKAGSVQFQWKDSLKVGVEYEAQAL 117

DB 61 NNTAWIOLKIRAPSNVSTVTHILYLPKAGSVQFQWKDSLKVGVEYEAQAL 117

RESULT 2

AAE13606
ID AAE13606 standard; protein; 589 AA.

XX AAE13606;

AC 26-FEB-2002 (first entry)

DE Mus musculus truncated reelin protein.

KW Mouse; reelin, F-spondin domain; CR-50 epitope; gene therapy; agyria;
polymicrogyria; ectopic gray matter.

XX Mus musculus.

PH Key Location/Qualifiers

FT Peptide 1..27

FT Protein /label= Signal_peptide

PN EPI149844-A2.

PD 31-OCT-2001.

PF 11-APR-2001; 2001EP-00303411.

PR 11-APR-2000; 2000JP-00109954.

PA (RIKE) RIKEN KK.

PI Mikoshiba K, Tabata H, Nakajima K;

DR WPI; 2002-019320/03.

XX N-PSDB; AAD22754.

PT Novel truncated Reelin protein containing F-spondin domain and CR-50
recognition site of Reelin protein, but not having Reelin repeat site,
useful to treat diseases including agyria due to abnormal neuron
alignment.

PS Claim 4; Page 26-30; 47pp; English.

XX The invention relates to a truncated Reelin protein comprising a F-
spondin domain and a CR-50 recognition site but no reelin protein repeat
site. Reelin is an essential molecule in developing a normal laminated
structure of cerebrum. The truncated reelin protein and its DNA are
useful for treating diseases including agyria, polymicrogyria, and
ectopic gray matter due to abnormal neuronal alignment. Truncated reelin
protein DNA is useful in gene therapy. The present sequence is Mus
musculus truncated reelin protein

XX SQ Sequence 589 AA;

Query Match 100.0%; Score 625; DB 5; Length 589;

Best Local Similarity 100.0%; Pred. No. 1.6e-63;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EOCGTIMGNNAVTFCEPYGPRLTTTCINTTASVLOFSIGSGCRFSYSDPSITVSAAK 60

DB 230 EOCGTIMGNNAVTFCEPYGPRLTTTCINTTASVLOFSIGSGCRFSYSDPSITVSAAK 289

QY 61 NNTAWIOLKIRAPSNVSTVTHILYLPKAGSVQFQWKDSLKVGVEYEAQAL 117

DB 230 NNTAWIOLKIRAPSNVSTVTHILYLPKAGSVQFQWKDSLKVGVEYEAQAL 346

RESULT 3

ABB05008
ID ABB05008 standard; protein; 3461 AA.

XX ABB05008;

DT 21-MAR-2002 (first entry)

XX Mouse reelin protein SEQ ID NO:2.

XX Mouse; reelin; low density lipoprotein receptor; LDLR; neuroprotective;
 KM extracellular glycoprotein; nocotropic; antilipemic; Alzheimer's disease;
 KM neurodegenerative disorder; neuronal regeneration; cognitive function;
 KM lipid metabolism disease; memory; developmental disorder.
 XX Mus musculus.
 OS
 XX US6323177-B1.
 PN
 XX 27-NOV-2001.
 PD
 XX 16-JUN-1999; 99US-00334220.
 PF
 XX 16-JUN-1999; 99US-00334220.
 PR
 XX (SUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PA
 XX Curran T, D'Arcangelo G;
 PI
 XX MPI: 2002-096596/13.
 DR
 XX N-PSDB; ABA92603.
 DR
 XX Novel composition useful for screening compounds that modulate Reelin
 PT binding to low density lipoprotein receptor, comprising an isolated
 PT Reelin polypeptide and low density lipoprotein receptor.
 PT
 XX Claim 16; Col 47-64; 45pp; English.
 PS
 XX The present invention describes a composition (I) comprising an isolated
 CC reelin protein (II) bound to an isolated low density lipoprotein receptor
 CC (LDLR) (III). (II) is an extracellular glycoprotein of approximately 385
 CC kDa containing a small region of similarity with F-glycophorin at the N
 CC terminus, a stretch of positively charged amino acids at the C terminus,
 CC and a series of eight internal repeats of 350-390 amino acids, each
 CC repeat containing two related sub-domains that flank a pattern of
 CC conserved cysteine residues known as an epidermal growth factor (EGF)-
 CC like motif. (I) has neuroprotective, nocotropic and antilipemic
 CC activities, and can be used as a modulator of reelin-LDLR interaction.
 CC (I) is useful in screen for compounds that modulate reelin binding to an
 CC LDLR, in an assay system, where the assay system comprises a microplate
 CC array and an automated robotic microprocessor controlled system for
 CC adding and removing reagents to the microplate array. The compounds
 CC identified by the above screening method are useful as therapeutic agents
 CC to provide or alleviate a diverse spectrum of diseases including
 CC neurodegenerative disorders such as Alzheimer's disease, to facilitate
 CC neuronal regeneration after injury, to prevent or alleviate lipid
 CC metabolism diseases, to enhance cognitive functions and memory or to
 CC ameliorate other developmental disorders. The present sequence represents
 CC mouse (Mus musculus) reelin, which is used in the exemplification of the
 CC present invention
 CC
 XX Sequence 3461 AA;
 SQ
 Query Match 100.0%; Score 625; DB 5; Length 3461;
 Best Local Similarity 100.0%; Pred. No. 1.9e-62;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EOCGTIMGNNAVTFCEPYGPRLTTTCLNTTASVLOFSIGSGSCFYSYSDPSITVSVAK 60
 DB 230 EOCGTIMGNNAVTFCEPYGPRLTTTCLNTTASVLOFSIGSGSCFYSYSDPSITVSVAK 289
 QY 61 NNTADMIOLEKTRAPSNVSTVHIILYLPBEAKGESVQFQKODSLAVGEVYECMAL 117
 DB 290 NNTADMIOLEKTRAPSNVSTVHIILYLPBEAKGESVQFQKODSLAVGEVYECMAL 346
 RESULT 4
 ID ABB57065 standard; protein; 3461 AA.
 XX ABB57065;
 AC
 XX

DT 07-MAR-2002 (first entry)
 DE Mouse ischemic condition related protein sequence SEQ ID NO:129.
 XX
 XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KM vasospastic ischaemia; ischemic condition; ischaemic disease.
 XX
 XX Mus musculus.
 OS
 XX WO200108188-A2.
 PN
 XX 22-NOV-2001.
 PD
 XX 18-MAY-2001; 2001WO-JP004192.
 PF
 XX 18-MAY-2001; 2000JP-00145977.
 PR
 XX (UYN-) UNIT NIHON SCHOOL JURIDICAL PERSON.
 PA
 XX Ishikawa K, Arai S, Takahashi Y, Nagata T, Ishii Y;
 PI
 XX MPI: 2002-034733/04.
 DR
 XX N-PSDB; ABI99284.
 DR
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 PT
 XX Claim 2; Page 385-400; 2690pp; English.
 PS
 XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 CC
 XX Sequence 3461 AA;
 SQ
 Query Match 100.0%; Score 625; DB 5; Length 3461;
 Best Local Similarity 100.0%; Pred. No. 1.9e-62;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EOCGTIMGNNAVTFCEPYGPRLTTTCLNTTASVLOFSIGSGSCFYSYSDPSITVSVAK 60
 DB 230 EOCGTIMGNNAVTFCEPYGPRLTTTCLNTTASVLOFSIGSGSCFYSYSDPSITVSVAK 289
 QY 61 NNTADMIOLEKTRAPSNVSTVHIILYLPBEAKGESVQFQKODSLAVGEVYECMAL 117
 DB 290 NNTADMIOLEKTRAPSNVSTVHIILYLPBEAKGESVQFQKODSLAVGEVYECMAL 346
 RESULT 5
 ID ADE60142 standard; protein; 3461 AA.
 XX ADE60142;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Rat Protein NP_035391, SEQ ID NO 6041.
 DE
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 KM

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XX Rattus norvegicus.
OS
XX WO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
PF
XX 14-AUG-2001; 2001US-0312147P.
PR
XX 01-NOV-2001; 2001US-0346382P.
PR
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO ) GEN HOSPITAL CORP.
PA
XX (FARB ) BAYER AG.
PA
XX Woolf C, D'urso D, Befort K, Costigan M;
PI
XX WPI: 2003-268312/26.
DR
XX GENBANK; NP_035391.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX Claim 1; Page; 1017pp; English.
PS
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3461 AA:
SQ
XX
XX Query Match 100.0%; Score 625; DB 7; Length 3461;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-62;
XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AC ADJ69818;
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human heat mitochondrial protein as a therapeutic target SegID1624.
DE
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
XX osteopathic; ophthalmological; cyostatic.
XX
XX Homo sapiens.
OS
XX
XX WO2003087768-A2.
XX
XX 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
PR
XX 17-JUN-2002; 2002US-0389987P.
PR
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA
XX (BUCK-) BUCK INST AGE RES.
PI
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX Warnock DE;
XX WPI: 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
PT
XX
XX Claim 1; SEQ ID NO 1624; 180pp; English.
PS
XX
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
XX Sequence 3427 AA:
SQ
XX
XX Query Match 91.5%; Score 572; DB 7; Length 3427;
XX Best Local Similarity 90.6%; Pred. No. 2.8e-56;
XX Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

AB05007
ID ABB05007 standard; protein; 3460 AA.
XX
AC ABB05007;
XX
DT 21-MAR-2002 (first entry)
XX
DE Human reelin protein SEQ ID NO:1.
XX
KW Human; reelin; low density lipoprotein receptor; LDLR; neuroprotective;
KM extracellular glycoprotein; nootropic; antilipemic; Alzheimer's disease;
KW neurodegenerative disorder; neuronal regeneration; cognitive function;
KM lipid metabolism disease; memory; developmental disorder.
XX
OS Homo sapiens.
XX
PN US6323177-B1.
XX
PD 27-NOV-2001.
XX
PF 16-JUN-1999; 99US-00334220.
XX
PR 16-JUN-1999; 99US-00334220.
XX
PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Curran T, D'arcangelo G;
XX
DR WPI; 2002-096596/13.
XX
DR N-PSDB; ABA92604.
XX
PT Novel composition useful for screening compounds that modulate Reelin
PT binding to low density lipoprotein receptor, comprising an isolated
PT Reelin polypeptide and low density lipoprotein receptor.
XX
PS Claim 16; Col 31-48; 45pp; English.
XX
CC The present invention describes a composition (I) comprising an isolated
CC reelin protein (II) bound to an isolated low density lipoprotein receptor
CC (LDLR) (III). (II) is an extracellular glycoprotein of approximately 385
CC kDa containing a small region of similarity with F-6pandin at the N
CC terminus, a stretch of positively charged amino acids at the C terminus,
CC and a series of eight internal repeats of 350-390 amino acids, each
CC repeat containing two related sub-domains that flank a pattern of
CC conserved cysteine residues known as an epidermal growth factor (EGF)-
CC like motif. (I) has neuroprotective, nootropic and antilipemic
CC activities, and can be used as a modulator of reelin-LDLR interaction.
CC (I) is useful in screen for compounds that modulate reelin binding to an
CC LDLR, in an assay system, where the assay system comprises a microplate
CC array and an automated robotic microprocessor controlled system for
CC adding and removing reagents to the microplate array. The compounds
CC identified by the above screening method are useful as therapeutic agents
CC to provide or alleviate a diverse spectrum of diseases including
CC neurodegenerative disorders such as Alzheimer's disease, to facilitate
CC neuronal regeneration after injury, to prevent or alleviate lipid
CC metabolism diseases, to enhance cognitive functions and memory or to
CC ameliorate other developmental disorders. The present sequence represents
CC human reelin, which is used in the exemplification of the present
CC invention
XX
SQ Sequence 3460 AA;

Query Match 91.5%; Score 572; DB 5; Length 3460;
Best Local Similarity 90.6%; Pred. No. 2.8e-56;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

61 NNTADMIOLEKIRAPSNVSTVTHILYLPBEAKGESVQFQKQDSLNGEYEAQMAL 117
1 EOCCTIMHGNAYFCEPYGPRELTTTCANTTASVLOFSIGSSGCFPSYSDPITTSYAK 60
229 EOCGALMHGNAVFCEPYGPRELTTTCANTTASVLOFSIGSSGCFPSYSDPITTVYAK 268

289 NNSADWIOLEKIRAPSNVSTVTHILYLPBEAKGESVQFQKQDSLNGEYEAQMAL 345

RESULT 8
ADE60143
ID ADE60143 standard; protein; 3460 AA.
XX
AC ADE60143;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P78509, SEQ ID NO 6043.
XX
KW Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
XX
DR GENBANK; P78509.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPRO at
CC ftp.wipro.int/pub/published_pct_sequences.
XX
SQ Sequence 3460 AA;

Query Match 91.5%; Score 572; DB 7; Length 3460;
Best Local Similarity 90.6%; Pred. No. 2.8e-56;

```
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 EOCGTIMGNATVFCBPYGPRLITTCINTTASVLOFSIGSGSCRFSPSPSTVSYAK 60
DB 229 EOCGAIMGNATVFCBPYGPRLITTCINTTASVLOFSIGSGSCRFSPSPSTVSYAK 288
QY 61 NNTADWIOLEKTRAPSNVSTVHILYLPEAKGESVOPQMKDSLRVGEVTEACMAL 117
DB 289 NNSADMIOLEKTRAPSNVSTVHILYLPEDAKGENVOPQMKENLRVGEVTEACMAL 345

RESULT 9
ADN95182
ID ADN95182 standard; protein; 3460 AA.
AC ADN95182;
XX
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human BEC/LBC-related protein sequence SegID104.
DE
XX growth; differentiation; blood endothelial cell; BEC;
XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
XX lymphatic growth agent; VEGF-D; antiangiogenic; cytostatic;
XX vasoactive; antiinflammatory; gene therapy; endothelial cell disorder;
XX inflammatory disease; cancer metastasis; lymphatic system; human.
XX
XX Homo sapiens.
XX
XX WO2003080640-A1.
XX
XX 02-OCT-2003.
XX
XX 07-MAR-2003; 2003WO-US006900.
XX
XX 07-MAR-2002; 2002US-0363019P.
XX
XX (LUDM-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
XX
XX Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX MPI: 2003-876899/81.
XX N-PSDB; ADN95183.
XX
XX Example 1; SEQ ID NO 104; 176pp; English.
XX
XX This invention relates to a method of differentially modulating the
XX growth or differentiation of blood endothelial cells (BEC) or lymphatic
XX endothelial cells (LEC) comprising contacting endothelial cells with a
XX composition comprising an agent that differentially modulates blood or
XX lymphatic endothelial cells. Treating hereditary lymphoedema comprises
XX identifying a human subject with lymphoedema and with a mutation in at
XX least one allele of a gene encoding a LEC protein, where the mutation
XX correlates with lymphoedema in human subjects, and with the proviso that
XX the LEC protein is not VEGFR-3; and administering to the subject a
XX composition comprising a lymphatic growth agent selected from VEGF-C or
XX VEGF-D polypeptides and polynucleotides. The invention may be useful for
XX the development of compounds with an antiangiogenic, cytostatic,
XX vasoactive or antiinflammatory activity or for gene therapy. The method
XX is useful in modulating the growth or differentiation of blood
XX endothelial cells or lymphatic endothelial cells, in treating hereditary
XX lymphoedema, in screening for an endothelial cell disorder or
XX predisposition to the disorder or in monitoring the efficacy or toxicity
XX of a drug on endothelial cells. The agent is useful in manufacturing a
XX medicament for the differential modulation of blood vessel endothelial
XX cell or lymphatic vessel endothelial cell growth or differentiation. The
XX lymphatic growth agent may also be used in manufacturing a medicament for
XX the treatment of hereditary lymphoedema resulting from a mutation in a
XX LEC gene or of other diseases involving the lymphatic vessels, such as
XX various inflammatory diseases and cancer metastasis via the lymphatic
XX system. The present sequence is that of a human BEC/BEC differentially
XX expressed protein which is related to the method of the invention.Note:
```

```
CC This sequence does not appear in the specification but was obtained by
CC the Indexer using the source data given in table 14 of the specification.
XX
XX Sequence 3460 AA;
SQ
QY Query Match 91.5%; Score 572; DB 7; Length 3460;
DB Best Local Similarity 90.6%; Pred. No.2.8e-56;
DB Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMGNATVFCBPYGPRLITTCINTTASVLOFSIGSGSCRFSPSPSTVSYAK 60
DB 229 EOCGAIMGNATVFCBPYGPRLITTCINTTASVLOFSIGSGSCRFSPSPSTVSYAK 288
QY 61 NNTADWIOLEKTRAPSNVSTVHILYLPEAKGESVOPQMKDSLRVGEVTEACMAL 117
DB 289 NNSADMIOLEKTRAPSNVSTVHILYLPEDAKGENVOPQMKENLRVGEVTEACMAL 345

RESULT 10
ADQ20919
ID ADQ20919 standard; protein; 3460 AA.
AC ADQ20919;
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 3739.
XX
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX PA Aziz N, Ginsburg WM, Zlocnik A;
XX PI MPI: 2004-441208/41.
XX N-PSDB; ADQ20919.
XX
XX Example 2; SEQ ID NO 3739; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
XX
XX Sequence 3460 AA;
SQ
QY Query Match 91.5%; Score 572; DB 8; Length 3460;
DB Best Local Similarity 90.6%; Pred. No.2.8e-56;
DB Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

QY 1 ECGTTMGNNAVTFCEPYGPRELTTTCLNTTASVLFQPSIGSGSCRFPSYSDPSITVSYAK 60
DB 229 ECGGAIMHGNAVTFCEPYGPRELTTTCLNTTASVLFQPSIGSGSCRFPSYSDPSITVLYAK 288
QY 61 NNTADMIQLEKTRAPNSVSTVTHILYLPBKAQGESVQFQMKDLSLVGEVYECMAL 117
DB 289 NNSADMIQLEKTRAPNSVSTVTHILYLPBKAQGENVOFQMKDLSLVGEVYECMAL 345

RESULT 11
ADQ88204
ID ADQ88204 standard; protein; 3460 AA.
XX
AC ADQ88204;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human 3533 protein, a reelin serine protease protein RELN.
XX
KW human; cardiovascular disorder; thrombotic disorder;
KW differential expression; gene therapy; aberrant vascularisation;
KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;
KW dyslipidaemia; high blood pressure; heart failure; cardiatic;
KW thrombolytic; anticoagulant; antilipemic; hypotensive; cardiatic;
KW reelin serine protease; RELN; EC 3.4.21; enzyme.
XX
OS Homo sapiens.
XX
PN WO2004063340-A2.
XX
PD 29-JUL-2004.
XX
PF 13-JAN-2004; 2004WO-US000393.
XX
PR 13-JAN-2003; 2003US-0439683P.
PR 05-FEB-2003; 2003US-0445216P.
PR 18-FEB-2003; 2003US-0448036P.
PR 12-MAR-2003; 2003US-0454189P.
PR 25-MAR-2003; 2003US-0457541P.
PR 29-APR-2003; 2003US-0466411P.
PR 08-MAY-2003; 2003US-0469041P.
PR 10-JUN-2003; 2003US-0477414P.
PR 13-JUN-2003; 2003US-0478560P.
PR 24-JUL-2003; 2003US-0489772P.
PR 28-JUL-2003; 2003US-0490660P.
PR 03-SEP-2003; 2003US-049838P.
PR 22-SEP-2003; 2003US-0504786P.
PR 24-SEP-2003; 2003US-0505570P.
PR 17-OCT-2003; 2003US-0512418P.
PR 27-OCT-2003; 2003US-0514660P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Stragliano NF, Healy A, Acton SL, Galvin KM, Donoghue MA,
PI Rogrigue-Way A, Tomlinson JE;
XX
PI WPI; 2004-553729/53.
XX
DR N-PSDB; ADQ88203.
XX
PT Identifying a compound for treating a cardiovascular or thrombotic
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
PT and detecting the binding.
XX
PS Claim 1; SEQ ID NO 46; 512pp; English.
XX
CC This invention relates to a novel compound that is capable of treating a
CC cardiovascular or thrombotic disorder. Specifically, it refers to the
CC identification of nucleic acid molecules, and the encoded proteins
CC thereof, which are differentially expressed in cardiovascular disease
CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of

CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation,
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,
CC dyslipidaemia, high blood pressure or heart failure. As such, they
CC exhibit cardiatic, thrombolytic, anticoagulant, antilipemic, hypotensive
CC and cardiatic activities. This polypeptide sequence is a human protein
CC that is differentially expressed in a patient with a cardiovascular
CC disorder, given in an exemplification of the invention.
XX
SQ Sequence 3460 AA;
XX
Query Match 91.5%; Score 572; DB 8; Length 3460;
Best Local Similarity 90.6%; Pred. No. 2.8e-56;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 ECGTTMGNNAVTFCEPYGPRELTTTCLNTTASVLFQPSIGSGSCRFPSYSDPSITVSYAK 60
DB 229 ECGGAIMHGNAVTFCEPYGPRELTTTCLNTTASVLFQPSIGSGSCRFPSYSDPSITVLYAK 288
QY 61 NNTADMIQLEKTRAPNSVSTVTHILYLPBKAQGESVQFQMKDLSLVGEVYECMAL 117
DB 289 NNSADMIQLEKTRAPNSVSTVTHILYLPBKAQGENVOFQMKDLSLVGEVYECMAL 345

RESULT 12
ABG25297
ID ABG25297 standard; protein; 3470 AA.
XX
AC ABG25297;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #25288.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
PI WPI; 2001-639362/73.
XX
DR N-PSDB; AAG89484.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 55656; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostic, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AB00010-AB030377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 3470 AA;
SQ

Query Match 91.5%; Score 572; DB 4; Length 3470;
Best Local Similarity 90.6%; Pred. No. 2.8e-56;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMGNNAVTFCEPYGPRELTTCTNTTASVLOFSISGSGCRFSSDPSITVSXK 60
DB 233 EOCGAIMGNAVTFCEPYGPRELTTCTNTTASVLOFSISGSGCRFSSDPSITVSXK 298
61 NNTADWIOLEKIRAPSNVSTVTHILYLPBEAKGESVOPQMKDSLAVGEVYACWAL 117
299 NNSADWIOLEKIRAPSNVSTVTHILYLPBEAKGESVOPQMKDSLAVGEVYACWAL 355

RESULT 13
AAE13605
ID AAE13605 standard; protein; 432 AA.
XX
AC AAE13605;
XX
DT 26-FEB-2002 (first entry)
XX
DE Xenopus laevis truncated reelin protein.
XX
KW Frog; reelin; F-spondin domain; CR-50 epitope; gene therapy; agyria;
XX polymicrogyria; ectopic gray matter.
XX
OS Xenopus laevis.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..432
FT /label= Mature_truncated_reelin_protein
XX
FN EPI149844-A2.
XX
PD 31-OCT-2001.
XX
PF 11-APR-2001; 2001EP-00303411.
XX
PR 11-APR-2000; 2000JP-00109954.
XX
PA (RIKE) RIKEN KK.
XX
PI Mikoshiba K, Tabata H, Nakajima K;
XX WPI; 2002-019320/03.
XX N-PSDB; AAD22753.
XX
DR WPI; 2002-019320/03.
XX
PT Novel truncated Reelin protein containing F-spondin domain and CR-50
PT recognition site of Reelin protein, but not having Reelin repeat site,
PT useful to treat diseases including agyria due to abnormal neuron
PT alignment.
XX
PS Claim 3; Page 16-19; 47p; English.
XX
CC The invention relates to a truncated Reelin protein comprising a F-
CC spondin domain and a CR-50 recognition site but no reelin protein repeat

CC site. Reelin is an essential molecule in developing a normal laminated
CC structure of cerebrum. The truncated reelin protein and its DNA are
CC useful for treating diseases including agyria, polymicrogyria, and
CC ectopic gray matter due to abnormal neuronal alignment. Truncated reelin
CC protein DNA is useful in gene therapy. The present sequence is Xenopus
CC laevis truncated reelin protein
XX

Sequence 432 AA;
SQ

Query Match 79.8%; Score 499; DB 5; Length 432;
Best Local Similarity 74.4%; Pred. No. 5.1e-49;
Matches 87; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 EOCGTIMGNNAVTFCEPYGPRELTTCTNTTASVLOFSISGSGCRFSSDPSITVSXK 60
DB 233 EOCGAIMGNAVTFCEPYGPRELTTCTNTTASVLOFSISGSGCRFSSDPSITVSXK 290
61 NNTADWIOLEKIRAPSNVSTVTHILYLPBEAKGESVOPQMKDSLAVGEVYACWAL 117
291 NNSSMPLERISAPSNVSTVTHILYLPBEAKGESVOPQMKDSLAVGEVYACWAL 347

RESULT 14
AAE13607
ID AAE13607 standard; protein; 623 AA.
XX
AC AAE13607;
XX
DT 26-FEB-2002 (first entry)
XX
DE Xenopus laevis intact reelin protein.
XX
KW Frog; reelin; F-spondin domain; CR-50 epitope; gene therapy; agyria;
XX polymicrogyria; ectopic gray matter.
XX
OS Xenopus laevis.
XX
FH Key Location/Qualifiers
FT Misc-difference 484
FT /note= "Encoded by CGA"
FT Misc-difference 495
FT /note= "Encoded by CAT"
XX
FN EPI149844-A2.
XX
PD 31-OCT-2001.
XX
PF 11-APR-2001; 2001EP-00303411.
XX
PR 11-APR-2000; 2000JP-00109954.
XX
PA (RIKE) RIKEN KK.
XX
PI Mikoshiba K, Tabata H, Nakajima K;
XX WPI; 2002-019320/03.
XX N-PSDB; AAD22779.
XX
DR WPI; 2002-019320/03.
XX
PT Novel truncated Reelin protein containing F-spondin domain and CR-50
PT recognition site of Reelin protein, but not having Reelin repeat site,
PT useful to treat diseases including agyria due to abnormal neuron
PT alignment.
XX
PS Example 1; Fig 1A; 47p; English.
XX
CC The invention relates to a truncated Reelin protein comprising a F-
CC spondin domain and a CR-50 recognition site but no reelin protein repeat
CC site. Reelin is an essential molecule in developing a normal laminated
CC structure of cerebrum. The truncated reelin protein and its DNA are
CC useful for treating diseases including agyria, polymicrogyria, and
CC ectopic gray matter due to abnormal neuronal alignment. Truncated reelin
CC protein DNA is useful in gene therapy. The present sequence is Xenopus
CC laevis intact reelin protein

XX Sequence 623 AA;
 SQ Query Match 79.8%; Score 499; DB 5; Length 623;
 Best Local Similarity 74.4%; Pred. No. 8.5e-49;
 Matches 87; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 ECGCTMHGNAVFCEPYPGRELTTCTNTTASVLOFSIGSGSCRPYSDEPITVSYAK 60
 DB 231 ECGALMHGNAVTFCDYGPRELITYQMTTASVLOFSIGSGSCRPYSDEPITVSYAK 230

QY 61 NNTADMTGLEKIRAPSNVSTVIHILYPEAKGESVQFQKODSLRVEVEACWAL 117
 DB 291 NNSGSMWPLERISAPSNVSTIIHILYPEAKGENVFRMRQENMQAGDYAEACWAL 347

RESULT 15
 ABO56700
 ID ABO56700 standard; protein; 84 AA.
 XX AC ABO56700;
 XX DT 29-JUL-2004 (first entry)
 XX DE Human genome derived single exon protein #2934.
 XX KM Human; gene expression; single exon probe; microarray;
 XX KM alternative splicing event; genomic alteration.
 XX OS Homo sapiens.
 XX PN US2003194704-A1.
 XX PD 16-OCT-2003.
 XX PF 03-APR-2002; 2002US-00029386.
 XX PR 03-APR-2002; 2002US-00029386.
 XX PA (PENN/) PENN S G.
 XX PA (RANK/) RANK D R.
 XX PA (HANK/) HANZEL D K.
 XX PI Penn SG, Rank DR, Hanzel DK;
 XX DR WPI, 2004-119264/12.
 XX PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX Claim 45; SEQ ID NO 30334; 80bp; English.

CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704

XX Sequence 84 AA;
 SQ Query Match 35.8%; Score 224; DB 8; Length 84;
 Best Local Similarity 88.9%; Pred. No. 6.1e-18;
 Matches 40; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 73 RAPSNTSVIHIILYPEAKGESVQFQKODSLRVEVEACWAL 117
 DB 3 RAPSNTSVIHIILYPEAKGENVQFQKODSLRVEVEACWAL 47

Search completed: August 4, 2005, 15:32:36
 Job time: 169 secs

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OM protein - protein search, using sw model

Run on: August 4, 2005, 15:27:08 ; Search time 43 Seconds
(without alignments)
203.115 Million cell updates/sec

Title: US-09-897-438B-2

Perfect score: 625

Sequence: 1 ECGRTIMGNNAVTFCEPYGP.....FQWKQDSLRYGEVYACMAL 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_5/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	3461	3	US-09-334-220-2
2	572	91.5	3460	3	US-09-334-220-1
3	81	13.0	616	4	US-09-236-063-1
4	81	13.0	640	3	US-09-351-814-13
5	70.5	11.3	568	4	US-09-248-796A-14918
6	68	10.9	462	4	US-09-583-110-3587
7	68	10.9	473	4	US-09-107-433-3273
8	68	10.9	884	4	US-09-902-540-13902
9	67.5	10.8	3623	4	US-09-341-461-2
10	67	10.7	339	4	US-09-802-371-2
11	67	10.7	356	4	US-09-489-039A-11918
12	66.5	10.6	569	4	US-09-514-245-22
13	66	10.6	658	1	US-08-409-995-5
14	66	10.6	658	3	US-08-685-467-5
15	66	10.6	658	3	US-08-913-942-5
16	66	10.6	658	4	US-09-684-707-5
17	66	10.6	1098	1	US-08-409-995-2
18	66	10.6	1098	1	US-08-685-467-2
19	66	10.6	1098	3	US-09-377-155-32
20	66	10.6	1098	3	US-08-913-942-2
21	66	10.6	1098	3	US-09-669-974-32
22	66	10.6	1098	3	US-09-258-347-44
23	66	10.6	1098	4	US-09-797-862-32
24	66	10.6	1098	4	US-09-684-707-2
25	65.5	10.5	126	4	US-09-603-208A-78
26	65.5	10.5	159	4	US-09-270-767-34992
27	65.5	10.5	159	4	US-09-270-767-50209

28	65.5	10.5	431	4	US-09-270-767-42950	Sequence 42950, A
29	65.5	10.5	540	4	US-09-538-092-793	Sequence 793, App
30	65.5	10.5	549	3	US-09-291-922-30	Sequence 30, App1
31	65	10.4	1187	1	US-08-201-697-2	Sequence 2, App1
32	64.5	10.3	213	2	US-08-716-284-2	Sequence 2, App1
33	64	10.2	533	4	US-09-302-540-13075	Sequence 13075, A
34	64	10.2	574	3	US-08-732-433-1	Sequence 1, App1
35	64	10.2	574	3	US-08-945-574-2	Sequence 2, App1
36	64	10.2	574	4	US-09-663-547B-2	Sequence 2, App1
37	63.5	10.2	280	4	US-09-248-796A-17297	Sequence 17297, A
38	63.5	10.2	337	2	US-08-923-856-4	Sequence 4, App1
39	63.5	10.2	337	3	US-09-216-294-4	Sequence 4, App1
40	63	10.1	148	4	US-09-252-991A-24972	Sequence 24972, A
41	63	10.1	382	1	US-08-049-282E-2	Sequence 2, App1
42	63	10.1	382	2	US-08-537-715-2	Sequence 2, App1
43	63	10.1	382	5	PCT-US94-04173-2	Sequence 2, App1
44	63	10.1	383	5	US-08-537-715-4	Sequence 4, App1
45	63	10.1	383	5	PCT-US94-04173-4	Sequence 4, App1
46	63	10.1	3913	4	US-09-949-016-10933	Sequence 10933, A
47	63	10.1	4377	4	US-09-949-016-6978	Sequence 6978, Ap
48	62.5	10.0	336	4	US-09-248-796A-17023	Sequence 17023, A
49	62.5	10.0	884	6	5208144-8	Patent No. 5208144
50	62.5	10.0	884	6	5208144-8	Patent No. 5208144
51	61.5	9.8	247	4	US-09-134-000C-6617	Sequence 6617, Ap
52	61.5	9.8	838	4	US-09-270-767-46665	Sequence 46665, A
53	61.5	9.8	1411	4	US-09-538-092-413	Sequence 413, App
54	61	9.8	375	4	US-08-978-404B-8	Sequence 8, App1
55	61	9.8	408	4	US-09-248-796A-16704	Sequence 16704, A
56	61	9.8	420	4	US-09-543-681A-6574	Sequence 6574, Ap
57	61	9.8	420	4	US-09-489-039A-8961	Sequence 8961, Ap
58	61	9.8	589	4	US-09-328-352-7592	Sequence 7592, Ap
59	61	9.8	1188	1	US-08-201-697-4	Sequence 4, App1
60	61	9.8	1246	4	US-09-949-016-8051	Sequence 8051, Ap
61	61	9.8	1246	4	US-09-949-016-8052	Sequence 8052, Ap
62	61	9.8	1246	4	US-09-949-016-8053	Sequence 8053, Ap
63	61	9.8	1246	4	US-09-949-016-8054	Sequence 8054, Ap
64	61	9.8	1246	4	US-09-949-016-8055	Sequence 8055, Ap
65	61	9.8	1274	4	US-09-949-016-8828	Sequence 8828, Ap
66	61	9.8	1274	4	US-09-949-016-8829	Sequence 8829, Ap
67	61	9.8	1274	4	US-09-949-016-8830	Sequence 8830, Ap
68	61	9.8	1274	4	US-09-949-016-8831	Sequence 8831, Ap
69	61	9.8	1274	4	US-09-949-016-8832	Sequence 8832, Ap
70	61	9.8	1749	4	US-09-640-419C-28	Sequence 28, App1
71	61	9.8	1839	2	US-09-172-977-4	Sequence 4, App1
72	61	9.8	1839	4	US-09-404-109-4	Sequence 4, App1
73	61	9.8	3924	4	US-09-538-092-1246	Sequence 1246, Ap
74	60.5	9.7	204	1	US-08-185-432-8	Sequence 8, App1
75	60.5	9.7	333	1	US-08-185-432-5	Sequence 5, App1
76	60.5	9.7	333	4	US-09-071-035-116	Sequence 116, App
77	60.5	9.7	406	4	US-09-071-035-114	Sequence 114, App
78	60.5	9.7	511	4	US-09-248-796A-16125	Sequence 16125, A
79	60.5	9.7	557	4	US-09-134-000C-4354	Sequence 4354, Ap
80	60.5	9.7	621	4	US-09-313-942-20	Sequence 20, App1
81	60.5	9.7	737	1	US-08-185-432-2	Sequence 2, App1
82	60.5	9.7	737	1	US-08-185-432-4	Sequence 4, App1
83	60.5	9.7	854	4	US-09-350-841A-1589	Sequence 1589, Ap
84	60.5	9.7	856	3	US-08-486-099-103	Sequence 103, App
85	60.5	9.7	856	3	US-08-484-223B-103	Sequence 103, App
86	60.5	9.7	856	3	US-08-919-597-103	Sequence 103, App
87	60.5	9.7	856	3	US-08-475-668A-103	Sequence 103, App
88	60.5	9.7	856	3	US-08-485-551A-103	Sequence 103, App
89	60.5	9.7	856	3	US-08-485-551A-103	Sequence 103, App
90	60.5	9.7	856	3	US-08-471-913A-103	Sequence 103, App
91	60.5	9.7	856	3	US-08-485-264A-103	Sequence 103, App
92	60.5	9.7	856	3	US-08-474-345A-103	Sequence 103, App
93	60.5	9.7	856	4	US-08-470-896-103	Sequence 103, App
94	60.5	9.7	856	4	US-08-485-546A-103	Sequence 103, App
95	60.5	9.7	856	4	US-08-487-266A-103	Sequence 103, App
96	60.5	9.7	857	1	US-08-320-151-10	Sequence 10, App1
97	60.5	9.7	857	1	US-08-413-116-10	Sequence 10, App1
98	60.5	9.7	857	3	US-08-804-439A-18	Sequence 18, App1
99	60.5	9.7	857	3	US-08-360-107A-113	Sequence 113, App
100	60.5	9.7	857	3	US-08-773-446-10	Sequence 10, App1
					US-08-720-229-18	Sequence 18, App1

ALIGNMENTS

RESULT 1
US-09-334-220-2

; Sequence 2, Application US/09334220

; Patent No. 6323177

; GENERAL INFORMATION:

; APPLICANT: St. Jude's Children's Research Hospital

; APPLICANT: Curran, Thomas

; APPLICANT: D'Arcangelo, Gabriella

; TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW

; TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND

; FILE REFERENCE: 2427/0704

; CURRENT APPLICATION NUMBER: US/09/334,220

; CURRENT FILING DATE: 1999-06-16

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 3461

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-334-220-2

Query Match 100.0%; Score 625; DB 3; Length 3461;

Best Local Similarity 100.0%; Pred. No. 1.5e-69;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EOCGITMAGNAVTFCEPYGPRELTTTCLNTTASVLOFSIGSGSCRFPSYSDPSITVSYAK 60

DB 230 EOCGITMAGNAVTFCEPYGPRELTTTCLNTTASVLOFSIGSGSCRFPSYSDPSITVSYAK 289

DB 290 NNTADWIOLEKIRAPNSVSTVHIILYLPBEAKGESVQFQMKDSLAVGEVYEAACMAL 346

RESULT 2

US-09-334-220-1

; Sequence 1, Application US/09334220

; Patent No. 6323177

; GENERAL INFORMATION:

; APPLICANT: St. Jude's Children's Research Hospital

; APPLICANT: Curran, Thomas

; APPLICANT: D'Arcangelo, Gabriella

; TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW

; TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND

; FILE REFERENCE: 2427/0704

; CURRENT APPLICATION NUMBER: US/09/334,220

; CURRENT FILING DATE: 1999-06-16

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 3460

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-334-220-1

Query Match 91.5%; Score 572; DB 3; Length 3460;

Best Local Similarity 90.6%; Pred. No. 8.8e-63;

Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGITMAGNAVTFCEPYGPRELTTTCLNTTASVLOFSIGSGSCRFPSYSDPSITVSYAK 60

DB 229 EOCGITMAGNAVTFCEPYGPRELTTTCLNTTASVLOFSIGSGSCRFPSYSDPSITVSYAK 288

QY 61 NNTADWIOLEKIRAPNSVSTVHIILYLPBEAKGESVQFQMKDSLAVGEVYEAACMAL 117

DB 289 NNTADWIOLEKIRAPNSVSTVHIILYLPBEAKGESVQFQMKDSLAVGEVYEAACMAL 345

RESULT 3
US-09-236-063-1

; Sequence 1, Application US/09236063

; Patent No. 6537792

; GENERAL INFORMATION:

; APPLICANT: Allen, Martin

; APPLICANT: Fang, Tsuei-Yun

; APPLICANT: Li, Yuxing

; APPLICANT: Liu, Hsuan-Liang

; APPLICANT: Chen, Hsui-Mei

; APPLICANT: Coutinho, Pedro

; APPLICANT: Hanzacko, Richard

; APPLICANT: Ford, Clark

; TITLE OF INVENTION: PROTEIN ENGINEERING OF GLUCOAMYLASE TO

; TITLE OF INVENTION: INCREASE PH OPTIMUM, SUBSTRATE SPECIFICITY AND

; TITLE OF INVENTION: THERMOSTABILITY

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Kohn & Associates

; STREET: 30500 No. 6537792thwestern Hwy.

; CITY: Farmington Hills

; STATE: Michigan

; COUNTRY: US

; ZIP: 48334

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/236,063

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Kohn, Kenneth I.

; REGISTRATION NUMBER: 30,955

; REFERENCE/DOCKET NUMBER: 0812.00001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (248) 539-5050

; TELEFAX: (248) 539-5055

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 616 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Aspergillus

US-09-236-063-1

Query Match 13.0%; Score 81; DB 4; Length 616;

Best Local Similarity 25.2%; Pred. No. 0.31;

Matches 34; Conservative 15; Mismatches 54; Indels 32; Gaps 4;

QY 9 GNAVTFCEPYGPRELTTTCLNTTASVLOFSIGSGSCRFPSYSDPSITVSYAK-- 61

DB 473 GGTITTAFTGSGSVSTSKTATNAKSTSTSTSTCTTPPAVAVTFDITATTGGENIT 532

QY 62 -----NTADWIOLEKIRAPNSVSTVHIILYLPBEAKGESVQF-----Q 99

DB 533 LVGSISQGLDWTSIGIALMSADKYSTSPIMWVVTLP---AGESPEYKFINESDSVE 589

QY 100 WKQDSLAVGEVYEAAC 114

DB 590 WESDPNRREYTPVQAC 604

RESULT 4

US-09-351-814-13

```

; Sequence 13, Application US/09351814
; Patent No. 6352851
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne Roenfeldt
; APPLICANT: Svendsen, Allan
; APPLICANT: Pedersen, Henrik
; APPLICANT: Vind, Jesper
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Frandsen, Torben Peter
; TITLE OF INVENTION: Glucosylase Variants
; FILE REFERENCE: 5636.200-US
; CURRENT APPLICATION NUMBER: US/09/351,814
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: PA 1998 00937
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PA 1998 01667
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: 60/093,528
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/115,545
; EARLIER FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PaetSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 640
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIGER
; US-09-351-814-13

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Query Match 13.0%; Score 81; DB 3; Length 640;
Best Local Similarity 25.2%; Pred. No. 0.32;
Matches 34; Conservative 15; Mismatches 54; Indels 32; Gaps 4;

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QY 9 GNAVTCEPYGRELTTCTTASVLPQSGSCRFYS-----DPSITVSYAKN-- 61
DB 497 GGTATTATPGSGSVSTSKTATYASKTSTSTSCCTPTAAVTFDLTATTYGENIY 556
QY 62 -----NTADWIOLEKIRAPSNVSTVIHILYLPBEAKGSEVQ-----Q 99
DB 557 LVGSIQGLDWEISDGLASADKRTSSDPLMYTVLP---AGESEFYKIRIESDSVE 613
QY 100 WKODSLRGEVYBAC 114
DB 614 WESDPNREYTVPOAC 628

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RESULT 5
US-09-248-796A-14918
; Sequence 14918, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14918
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-14918

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Query Match 11.3%; Score 70.5; DB 4; Length 568;
Best Local Similarity 31.5%; Pred. No. 5.9;
Matches 23; Conservative 16; Mismatches 15; Indels 19; Gaps 5;
QY 45 CRPSYSDPSITVSYAKNT-----ADWIOLEKIRAPSNVSTVIHILYLPBEAKGSEVQ 97

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DB 250 CKFTYDDAIR-AYA-NTLBEGIKYKDWTONIDKSNAPNNV-----EPQESLJK 297
QY 98 PQWKODSLRGEVY 110
DB 298 VKFDKYSIFVQGL 310

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RESULT 6
US-09-583-110-3587
; Sequence 3587, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3587
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-3587

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Query Match 10.9%; Score 68; DB 4; Length 462;
Best Local Similarity 24.6%; Pred. No. 9.1;
Matches 30; Conservative 16; Mismatches 42; Indels 34; Gaps 6;

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QY 6 IMHNAVTCEP-----YGPRLTTCCLNTTAA---SVLPQSGSCRFYS 50
DB 70 IFSKDVLFSTPSIKLHLRLISYAKKEGTETALGTKDMLGSKIMSGFGLSGISRF 129
QY 51 DPSI---TYSYAKNTADWIOLEKIRAPSNVSTVIHILYLPBEAKGSEVQ 97
DB 130 VPSVLTRTVSQSFR-----MWSKV-VPOKEEDLHLMNQPIYQVLMTPPESEKRAAD 183
QY 98 PQ 99
DB 184 FE 185

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RESULT 7
US-09-107-433-3273
; Sequence 3273, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; FILE REFERENCE: 5206
; CURRENT APPLICATION NUMBER: US/09/107,433
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; APPLICATION DATA:

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Query Match 10.7%; Score 67; DB 4; Length 339;
Best Local Similarity 24.3%; Pred. No. 7.7;
Matches 25; Conservative 21; Mismatches 39; Indels 18; Gaps 4;
QY 2 QCGTTHGNAVTCEPCEPRLTTTCNTTASVLOFSIGSGCRFSYSDPSITVSANKNTA---SDPSITV--- 56
DB 112 QALIKRGSILKCDLFSRRKPCSA-----LKNIVAGVIRISYWPADPEISLITE 163
QY 57 -SYAKNNTADWIOLEKIRAPSNVSTVHILYLPKAGSVOF 98
DB 164 ASSEDEKADAKAVERLKSNSRA---HVCVLQPLVCYMWQF 202

RESULT 11
US-09-489-039A-11918
; Sequence 11918, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11918
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11918

Query Match 10.7%; Score 67; DB 4; Length 356;
Best Local Similarity 26.3%; Pred. No. 8.3;
Matches 31; Conservative 19; Mismatches 56; Indels 12; Gaps 4;
QY 9 GNAVTCCEPCEPRLTTTCNTTASVLOFSIGSGCRFSYSDPSITVSANKNTA---DWI 67
DB 238 GGAIAPKAGVOPLPVPTGNDATIALQULIT-AGDQNTISKSEIYVAAAANKVAVDFI 296
QY 68 QLEKIRAPSNVSTVHILYLPKAGSVOF-----WKDSLKVGVEYECMNL 117
DB 297 QGKKPQASTLVNTPSQLFTPEVVTANIKAEIFDKKIQTW--DQVSGEYAAACQYL 352

RESULT 12
US-09-514-245-22
; Sequence 22, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTTET, Beelyne
; APPLICANT: ARNAUD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Type B PWD circovirus

US-09-514-245-22
Query Match 10.6%; Score 66.5; DB 4; Length 569;
Best Local Similarity 24.4%; Pred. No. 19;
Matches 32; Conservative 14; Mismatches 34; Indels 51; Gaps 8;
QY 5 TTHGNAVTCEPCEPRLTTTCNTTASVLOFSIGSGCRFSYSDPSITVSANKNTA--- 61
DB 222 TTFHNNNVIAIAQGP-----IIQSQTSIWQ-----SYL--SFTSSYKQGAT 263
QY 62 -----NTADWIOLEKIRAPSN-----SVTVHILY-LPEAKGESVOF 100
DB 264 NONGAILGROFPVGSYSDPSYFSKI--PNSGQYKPLISCFGLFPALBDGKGGMARFKW 321
QY 101 -----KQDS 104
DB 322 IFWIVSDKQDS 332

RESULT 13
US-08-409-995-5
; Sequence 5, Application US/08409995
; Patent No. 5646259
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen I.
; APPLICANT: St. Geme III, Joseph W.
; TITLE OF INVENTION: Haemophilus Adhesion Proteins
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,995
; FILING DATE: 24-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61053/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
US-08-409-995-5

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QY 46 RFSYSDPSITVSANKNTADWIOLEKIRAPSNVSTVYIHI 84
DB 188 AGATTTPKAVNT-----STTDGLKFAKDAGANGDTTVHL 222

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RESULT 14
US-08-685-467-5
: Sequence 5, Application US/08685467
: Patent No. 6060059
: GENERAL INFORMATION:
: APPLICANT: St. Gene III, Joseph W.
: APPLICANT: Barenkamp, Stephen J.
: TITLE OF INVENTION: HAEMOPHIUS ADHESION PROTEINS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
: STREET: Four Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: United States
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/685.467
: FILING DATE: 22-JUL-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/409,995
: FILING DATE: 24-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Silva, Robin M.
: REGISTRATION NUMBER: 38,304
: REFERENCE/DOCKET NUMBER: A-61053-2/RFT/RMS
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELEX: 910 277299
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 658 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: US-08-685-467-5

Query Match 10.6%; Score 66; DB 3; Length 658;
Best Local Similarity 24.2%; Pred. NO. 28;
Matches 24; Conservative 19; Mismatches 36; Indels 20; Gaps 4

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: Sequence 5, Application US/08913942
: Patent No. 6200578
: GENERAL INFORMATION:
: APPLICANT: St. Gene, Joseph
: APPLICANT: Barenkamp, Stephen J.
: TITLE OF INVENTION: HAEMOPHIUS ADHESION PROTEINS
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
: STREET: Four Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: United States

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      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      OPERATING SYSTEM: PC-DOS/MS-DOS
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      FILING DATE: 29-DEC-1997
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      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/409,995
      FILING DATE: 24-MAR-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: PCT/US96/4031
      FILING DATE: 22-MAR-1996
      ATTORNEY/AGENT INFORMATION:
      NAME: Vance, Dolly A.
      REGISTRATION NUMBER: 39,054
      REFERENCE/DOCKET NUMBER: A-61053-1/RPT/RMS/DAV
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 781-1989
      TELEFAX: (415) 398-3249
      TELEX: 910 277239
      INFORMATION FOR SEQ ID NO: 5:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 658 amino acids
      TYPE: amino acid
      STRANDEDNESS: unknown
      TOPOLOGY: unknown
      MOLECULE TYPE: protein
      US-08-913-942-5

Query Match          10.6%; Score 66; DB 3; Length 658;
Best Local Similarity 24.2%; Pred. No. 28;
Matches    24; Conservative   19; Mismatches   36; Indels   20; Gaps    4

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Best Local Similarity 24.2%; Pred. No. 28;
Matches 24; Conservative 19; Mismatches 36; Indels 20; Gaps 4

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Search completed: August 4, 2005, 15:37:01
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 15:35:34 ; Search time 158 Seconds
(without alignments)
289.092 Million cell updates/sec

Title: US-09-897-438b-2

Perfect score: 625

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	572	91.5	3460	10 US-10-723-860-3739	Sequence 3739, Ap
5	572	91.5	3460	17 US-10-753-267-46	Sequence 46, Appl
6	572	91.5	432	10 US-11-019-829-22	Sequence 22, Appl
7	499	79.8	432	10 US-09-832-189a-2	Sequence 2, Appl1
8	224	35.8	84	14 US-10-029-386-3034	Sequence 3034, A
9	190	30.4	70	4 US-09-864-761-47165	Sequence 47165, A
10	107	17.1	28	9 US-09-864-761-44551	Sequence 44551, A
11	83	13.3	316	16 US-10-767-701-32303	Sequence 32303, A

12	81	13.0	640	14 US-10-038-723-13	Sequence 13, Appl
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15	74	11.8	639	18 US-10-991-654-5	Sequence 5, Appl
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17	73	11.7	1095	14 US-10-228-063-45	Sequence 45, Appl
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78	65.5	10.5	549	13 US-10-051-902-30	Sequence 30, Appl
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86 65 10.4 295 16 US-10-425-115-233981 Sequence 233981,
87 65 10.4 438 9 US-09-738-626-6703 Sequence 6703, Ap
88 65 10.4 451 14 US-09-712-363-171 Sequence 171, App
89 65 10.4 451 14 US-10-080-170-400 Sequence 400, App
90 65 10.4 451 14 US-10-080-170-400 Sequence 400, App
91 65 10.4 451 16 US-10-468-356-400 Sequence 400, App
92 65 10.4 4823 15 US-10-051-874-159 Sequence 159, App
93 64.5 10.3 109 16 US-10-437-963-118926 Sequence 118926,
94 64.5 10.3 389 15 US-10-425-114-54288 Sequence 10499, A
95 64.5 10.3 550 9 US-09-815-242-10499 Sequence 10499, A
96 64.5 10.3 559 16 US-10-425-115-321798 Sequence 321798,
97 64.5 10.3 599 14 US-10-138-075-5 Sequence 5, Appli
98 64.5 10.3 599 16 US-10-739-930-10739 Sequence 10739, A
99 64.5 10.3 507 16 US-10-437-963-196952 Sequence 196952,
100 64.5 10.3 1001 16 US-10-437-963-196954 Sequence 196954,

ALIGNMENTS

RESULT 1
US-09-897-438B-2
; Sequence 2, Application US/09897438B
; Patent No. US20020137095A1
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsumihiro
; APPLICANT: Tate, Naoko
; TITLE OF INVENTION: REELIN PROTEIN CR-50 EPI TOPE REGION
; FILE REFERENCE: 04853-0076-00000
; CURRENT APPLICATION NUMBER: US/09/897,438B
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP 2000-202801
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
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DB 61 NNTADWIOLEKIRAPSNVSTVHIILYLPEBAKGSVQFQWKODSLRVGEVYEAACMAL 117
RESULT 2
US-09-832-189A-4
; Sequence 4, Application US/09832189A
; Publication No. US20030114657A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; TITLE OF INVENTION: Truncated Reelin Protein and DNA Encoding the Same
; FILE REFERENCE: PH-1167
; CURRENT APPLICATION NUMBER: US/09/832,189A
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: JP 2000-109954
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-832-189A-4
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Best Local Similarity 100.0%; Pred. No. 2,8e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Brian D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1624
; LENGTH: 3427
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124,
; LOCATION: 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136,
; LOCATION: 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148,
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; OTHER INFORMATION: Xaa = Any Amino Acid
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DB 289 NNSADWIOLEKIRAPSNVSTVHIILYLPEBAKGSVQFQWKODSLRVGEVYEAACMAL 345
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US-10-723-860-3739
; Sequence 3739, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natascha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods of Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPIS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26

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; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 3739
; LENGTH: 3460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-3739

Query Match      91.5%; Score 572; DB 16; Length 3460;
Best Local Similarity 90.6%; Pred. No. 3.9e-56;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      1 EOCGTIMHGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGSCRFSSDPSITVSYAK 60
DB      229 EOCGAIMHGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGSCRFSSDPSITVLYAK 288

QY      61 NNTADWIOLEKIRAPSNVSTVTHIILYPEKNGESVQFQWKODSLRVEVYEAQMAL 117
DB      289 NNSADWIOLEKIRAPSNVSTIHIILYPEKNGESVQFQWKODSLRVEVYEAQMAL 345

RESULT 5
US-10-753-267-46
; Sequence 46, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriquez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12822, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MP103-003P1RNMNM
; CURRENT APPLICATION NUMBER: US/10753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 3460
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-46

Query Match      91.5%; Score 572; DB 17; Length 3460;
Best Local Similarity 90.6%; Pred. No. 3.9e-56;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      1 EOCGTIMHGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGSCRFSSDPSITVSYAK 60
DB      229 EOCGAIMHGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGSCRFSSDPSITVLYAK 288

QY      61 NNTADWIOLEKIRAPSNVSTVTHIILYPEKNGESVQFQWKODSLRVEVYEAQMAL 117
DB      289 NNSADWIOLEKIRAPSNVSTIHIILYPEKNGESVQFQWKODSLRVEVYEAQMAL 345

RESULT 6
US-11-019-829-22
; Sequence 22, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 3460
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: reelin (RELN)
; LOCATION: (1)..(3460)
; OTHER INFORMATION: U79716
US-11-019-829-22

Query Match      91.5%; Score 572; DB 20; Length 3460;
Best Local Similarity 90.6%; Pred. No. 3.9e-56;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      1 EOCGTIMHGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGSCRFSSDPSITVSYAK 60
DB      229 EOCGAIMHGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGSCRFSSDPSITVLYAK 288

QY      61 NNTADWIOLEKIRAPSNVSTVTHIILYPEKNGESVQFQWKODSLRVEVYEAQMAL 117
DB      289 NNSADWIOLEKIRAPSNVSTIHIILYPEKNGESVQFQWKODSLRVEVYEAQMAL 345

RESULT 7
US-09-832-189A-2
; Sequence 2, Application US/09832189A
; Publication No. US20030114657A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; TITLE OF INVENTION: Truncated Reelin Protein and DNA Encoding the Same
; FILE REFERENCE: PH-1167
; CURRENT APPLICATION NUMBER: US/09/832,189A
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: JP 2000-109954
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-832-189A-2

Query Match      79.8%; Score 499; DB 10; Length 432;
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Best Local Similarity 74.4%; Pred. No. 7.5e+49;
Matches 87; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 EOCGIMGNAYTFCBPYGPRLITTCMTTASVLOFISGSCRFPSYSDSITVSYAK 60
Db 231 EOCGIMHGAATVFCBPYGPRLITTCMTTASVLOFISGSCRFPSYSDSITVSYAK 290

QY 61 NNTADWIOLEKTRAPSNVSTVTHILYLPBEAKGESVQFQKODSLRGEVYEACMAL 117
Db 291 NNTSSMPLERISAPSNVSTVTHILYLPBEAKGENVCFRMOENLMOAGDYVEACMAL 347

RESULT 8
US-10-029-386-30334
; Sequence 30334, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30334
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR7.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
; OTHER INFORMATION: SWISSPROT HIT: O14063, EVALUE 2.00e+00
US-10-029-386-30334

Query Match 35.8%; Score 224; DB 14; Length 84;
Best Local Similarity 88.9%; Pred. No. 6.7e-18;
Matches 40; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 73 RAPSNVSTVTHILYLPBEAKGESVQFQKODSLRGEVYEACMAL 117
Db 3 RAPSNVSTVTHILYLPBEAKGENVCFRMOENLMOAGDYVEACMAL 47

RESULT 9
US-09-864-761-47165
; Sequence 47165, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47165
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000121.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: O14063, EVALUE 1.20e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE938667.1, EVALUE 2.00e-22
US-09-864-761-47165

Query Match 30.4%; Score 190; DB 9; Length 70;
Best Local Similarity 86.8%; Pred. No. 4.6e-14;
Matches 33; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 80 TVTHILYLPBEAKGESVQFQKODSLRGEVYEACMAL 117
Db 1 TVTHILYLPBEAKGENVCFRMOENLMOAGDYVEACMAL 38

RESULT 10
US-09-864-761-44551
; Sequence 44551, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44551
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000121.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.44
; OTHER INFORMATION: SWISSPROT HIT: P76008, EVALU 2.90e+00
; US-09-864-761-44551

Query Match      17.1%; Score 107; DB 9; Length 28;
Best Local Similarity 94.7%; Pred. No. 5.9e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EOCGTIMGNATVFCPEY 19
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Db      10 EOCGAIMGNATVFCPEY 28

RESULT 11
US-10-767-701-32303
; Sequence 32303; Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(5353)B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 32303
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(316)
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; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C124217_1.pcp
; US-10-767-701-32303

Query Match      13.3%; Score 83; DB 16; Length 316;
Best Local Similarity 25.2%; Pred. No. 0.84;
Matches 34; Conservative 15; Mismatches 54; Indels 32; Gaps 4;

QY      9 GNAVFCBPYGRRLTTCANTTASVLOPSIGSGCRFSYS-----DSITVSYAKN-- 61
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Db      172 GGTATATPTGSGSVSTSKTATASKTSTSSASCTTPTAAVTFDLATTTGENTY 231
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QY      62 -----NTADWIOLEKIRAPSNVSTVHILVLPBEAKGESVQF-----Q 99
        |||||
Db      232 LVGSISQLGDWETSDDIALSADKYTSSDPLMYVTLP---AGESEFYKFRIESDDSV 288
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QY      100 WKODSLRAGEVYEAC 114
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Db      289 WESDPNREYTVPOAC 303

RESULT 12
US-10-038-723-13
; Sequence 13; Application US/10038723
; Publication No. US20030032163A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne Roenfeldt
; APPLICANT: Svendsen, Allan
; APPLICANT: Pedersen, Henrik
; APPLICANT: Vind, Jesper
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Frandsen, Torben Peter
; TITLE OF INVENTION: Glucosylase Variants
; FILE REFERENCE: 5636.200-US
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US/10/038,723
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/351,814
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: PA 1998 00937
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 01667
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,528
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/115,545
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 640
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIGER
; US-10-038-723-13

Query Match      13.0%; Score 81; DB 14; Length 640;
Best Local Similarity 25.2%; Pred. No. 3.6;
Matches 34; Conservative 15; Mismatches 54; Indels 32; Gaps 4;

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Db      497 GGTATATPTGSGSVSTSKTATASKTSTSSASCTTPTAAVTFDLATTTGENTY 556
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QY      62 -----NTADWIOLEKIRAPSNVSTVHILVLPBEAKGESVQF-----Q 99
        |||||
Db      557 LVGSISQLGDWETSDDIALSADKYTSSDPLMYVTLP---AGESEFYKFRIESDDSV 613
        |||||

QY      100 WKODSLRAGEVYEAC 114
        |||||
Db      614 WESDPNREYTVPOAC 628

RESULT 13
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OM protein - protein search, using sw model

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Maximum Match 100%

Listing first 100 summaries

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22: /cgn2_6/prodata/1/paa/US098_COMB.pep:*

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29: /cgn2_6/prodata/1/paa/US103_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	625	100.0	117	23	US-09-897-438B-2	Sequence 2, Appli
2	625	100.0	589	23	US-09-832-189A-4	Sequence 4, Appli
3	625	100.0	3461	28	US-10-219-051B-6041	Sequence 6041, Ap
4	572	91.5	2119	21	US-09-724-676-78129	Sequence 78129, A
5	572	91.5	2119	21	US-09-724-676A-78129	Sequence 81, Appl
6	572	91.5	2830	37	US-60-245-221-81	Sequence 28, Appl
7	572	91.5	2830	37	US-60-258-279-28	Sequence 3671, Ap
8	572	91.5	2954	24	US-09-949-003C-3671	Sequence 37739, A
9	572	91.5	2992	27	US-10-170-205E-37739	Sequence 10999, A
10	572	91.5	2992	37	US-60-453-050-10999	Sequence 10999, A
11	572	91.5	2992	37	US-60-453-135-10999	Sequence 10999, A
12	572	91.5	2992	37	US-60-466-412-10999	Sequence 10999, A
13	572	91.5	3107	21	US-09-724-676-78128	Sequence 78128, A
14	572	91.5	3107	21	US-09-724-676A-78128	Sequence 1624, Ap
15	572	91.5	3427	30	US-10-408-765-1624	Sequence 1624, Ap
16	572	91.5	3427	30	US-10-408-765A-1624	Sequence 1624, Ap
17	572	91.5	3427	37	US-60-389-987-1624	Sequence 1624, Ap
18	572	91.5	3427	37	US-60-412-418-1624	Sequence 1624, Ap
19	572	91.5	3460	1	PCT-US03-38193-3739	Sequence 3739, Ap
20	572	91.5	3460	1	PCT-US04-00393-46	Sequence 46, Appl
21	572	91.5	3460	24	US-09-949-003C-2384	Sequence 2384, Ap
22	572	91.5	3460	28	US-10-219-051B-6043	Sequence 6043, Ap
23	572	91.5	3460	31	US-10-505-928-104	Sequence 104, App
24	572	91.5	3460	33	US-10-723-860-3739	Sequence 3739, Ap
25	572	91.5	3460	33	US-10-753-267-46	Sequence 46, Appl
26	572	91.5	3460	36	US-11-019-829-22	Sequence 22, Appl
27	572	91.5	3470	1	PCT-US01-08631-55656	Sequence 55656, A
28	499	79.8	432	23	US-09-832-189A-2	Sequence 2, Appli
29	224	35.8	84	26	US-10-029-386-30334	Sequence 30334, A
30	190	30.4	70	23	US-09-864-761-47165	Sequence 47165, A
31	190	30.4	70	28	US-10-203-135-33869	Sequence 33869, A
32	109.5	17.5	1504	21	US-09-724-676-78132	Sequence 78132, A
33	109.5	17.5	1504	21	US-09-724-676A-78132	Sequence 78132, A
34	109.5	17.5	2492	21	US-09-724-676-78131	Sequence 78131, A
35	109.5	17.5	2492	21	US-09-724-676A-78131	Sequence 78130, A
36	109.5	17.5	2863	21	US-09-724-676-78130	Sequence 78130, A
37	109.5	17.5	2863	21	US-09-724-676A-78130	Sequence 78130, A
38	107	17.1	28	23	US-09-864-761-44551	Sequence 44551, A
39	107	17.1	28	27	US-10-182-993-33489	Sequence 33489, A
40	107	17.1	28	27	US-10-203-134-34447	Sequence 34447, A
41	107	17.1	28	28	US-10-203-135-33725	Sequence 33725, A
42	107	17.1	28	28	US-10-203-136-34566	Sequence 34566, A
43	83	13.3	316	33	US-10-767-701-32303	Sequence 32303, A
44	82.5	13.2	1027	37	US-60-230-435-1085	Sequence 1085, Ap
45	82.5	13.2	1169	37	US-60-212-656-449	Sequence 449, App
46	81.5	13.0	1468	1	PCT-US01-08631-55654	Sequence 55654, A
47	81.5	13.0	1789	37	US-60-207-315-370	Sequence 370, App
48	81.5	13.0	1789	37	US-60-230-435-1413	Sequence 1413, Ap
49	81	13.0	614	22	US-09-791-537-78148	Sequence 78148, A
50	81	13.0	616	1	PCT-US00-00532-1	Sequence 1, Appli
51	81	13.0	640	1	PCT-US04-13841-4	Sequence 4, Appli
52	81	13.0	640	20	US-09-612-489-13	Sequence 13, Appl
53	81	13.0	640	22	US-09-791-537-113621	Sequence 113621, A
54	81	13.0	640	26	US-10-038-723-13	Sequence 13, Appl
55	81	13.0	640	30	US-10-421-586-14	Sequence 14, Appl
56	77	12.3	574	1	PCT-US04-10229-118	Sequence 118, App
57	75	12.0	86	33	US-10-767-795-81672	Sequence 81672, A
58	74.5	11.9	834	1	PCT-US01-08631-55655	Sequence 55655, A
59	74	11.8	639	22	US-09-791-537-113620	Sequence 113620, A
60	74	11.8	640	22	US-09-791-537-152797	Sequence 152797, A
61	73	11.7	139	30	US-10-424-599-212843	Sequence 212843, A
62	73	11.7	639	22	US-09-791-537-113623	Sequence 113623, A
63	73	11.7	1095	1	PCT-US02-27129-45	Sequence 45, Appl
64	73	11.7	1095	1	PCT-US04-07182A-45	Sequence 45, Appl
65	73	11.7	1095	28	US-10-228-063-45	Sequence 45, Appl
66	72	11.5	208	28	US-10-219-999-59707	Sequence 59707, A
67	72	11.5	208	30	US-10-425-114-71644	Sequence 71644, A
68	72	11.5	208	30	US-10-425-114A-71644	Sequence 71644, A
69	72	11.5	208	37	US-60-324-109-25684	Sequence 25684, A

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70 72 11.5 247 30 US-10-425-115-229189
71 72 11.5 285 21 US-09-708-427-83672
72 72 11.5 350 21 US-09-708-427-83671
73 72 11.5 405 21 US-09-708-427-83670
74 71.5 11.4 91 26 US-10-029-386-29362
75 71 11.4 197 26 US-10-078-725-169
76 71 11.4 197 26 US-60-270-153-169
77 71 11.4 455 1 PCT-US99-22855-2315
78 71 11.4 457 1 PCT-US99-22855-2314
79 71 11.4 482 1 PCT-US99-22855-2313
80 71 11.4 1051 30 US-10-425-115-338413
81 71 11.4 1201 30 US-60-638-099-14321
82 70.5 11.3 271 30 US-10-415-182A-9116
83 70.5 11.3 279 30 US-10-415-182A-1146
84 70.5 11.3 400 27 US-10-179-131-8170
85 70.5 11.3 568 32 US-10-603-113-14918
86 70.5 11.3 568 37 US-60-096-409-14918
87 70.5 11.3 577 28 US-10-219-999-36487
88 70.5 11.3 577 30 US-10-425-114-43051
89 70.5 11.3 577 30 US-10-425-114A-43051
90 70.5 11.3 577 37 US-10-424-109-22439
91 70.5 11.3 901 30 US-10-424-109-193645
92 70 11.2 222 34 US-10-857-673-12
93 70 11.2 224 34 US-10-857-673-4
94 70 11.2 366 28 US-10-219-999-47541
95 70 11.2 366 30 US-10-425-114-56131
96 70 11.2 366 30 US-10-425-114A-56131
97 70 11.2 366 37 US-60-324-109-30959
98 70 11.2 593 30 US-10-424-599-222406
99 70 11.2 809 34 US-10-857-673-2
100 70 11.2 809 34 US-10-857-673-15
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ALIGNMENTS

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Sequence 229189,
Sequence 83672, A
Sequence 83671, A
Sequence 83670, A
Sequence 29362, A
Sequence 169, App
Sequence 2315, App
Sequence 2314, App
Sequence 2313, App
Sequence 14321, A
Sequence 9116, App
Sequence 1146, App
Sequence 8170, App
Sequence 14918, A
Sequence 14918, A
Sequence 36487, A
Sequence 43051, A
Sequence 22439, A
Sequence 193645,
Sequence 12, Appl
Sequence 4, Appl
Sequence 47541, A
Sequence 56131, A
Sequence 56131, A
Sequence 30959, A
Sequence 222406,
Sequence 2, Appl
Sequence 15, Appl
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RESULT 1
US-09-897-438b-2
; Sequence 2, Application US/09897438B
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
; APPLICANT: Tate, Naoko
; TITLE OF INVENTION: REELIN PROTEIN CR-50 EPI TOBE REGION
; FILE REFERENCE: 04853-0076-00000
; CURRENT APPLICATION NUMBER: US/09/897,438B
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: JP 2000-202801
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-897-438b-2
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Query Match 100.0%; Score 625; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-66;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 EOCGTMGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGCRFSYSDPSITVSVAK 60
QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVGEVYACMAL 117
DB 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVGEVYACMAL 117
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RESULT 2
US-09-832-189A-4
; Sequence 4, Application US/09832189A
; GENERAL INFORMATION:
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; APPLICANT: RIKEN
; TITLE OF INVENTION: Truncated Reelin Protein and DNA Encoding the Same
; FILE REFERENCE: PH-1167
; CURRENT APPLICATION NUMBER: US/09/832,189A
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: JP 2000-109954
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-832-189A-4

Query Match 100.0%; Score 625; DB 23; Length 589;
Best Local Similarity 100.0%; Pred. No. 1.8e-65;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 230 EOCGTMGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGCRFSYSDPSITVSVAK 289
QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVGEVYACMAL 117
DB 290 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVGEVYACMAL 346
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RESULT 3
US-10-219-051B-6041
; Sequence 6041, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 6041
; LENGTH: 3461
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_035391
; DATABASE ENTRY DATE: 2002-09-19
US-10-219-051B-6041
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Query Match 100.0%; Score 625; DB 28; Length 3461;
Best Local Similarity 100.0%; Pred. No. 2.1e-64;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EOCGTMGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGCRFSYSDPSITVSVAK 60
DB 230 EOCGTMGNNAVTFCEPYGPRELTTTCNTTTASVLOFSIGSGCRFSYSDPSITVSVAK 289
QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVGEVYACMAL 117
DB 290 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVGEVYACMAL 346
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RESULT 4
US-09-724-676-78129
; Sequence 78129, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
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Query Match          91.5%; Score 572; DB 24; Length 2954;
Best Local Similarity 90.6%; Pred. No. 4.2e-58;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVSXAK 60
DB 142 EOCGAIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVLVYAK 201

QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVEGYEACMAL 117
DB 202 NNSADMIOLEKIRAPSNVSTIHIILYLPEDAKGENVQFQKODSLRVEGYEACMAL 258

RESULT 9
US-10-170-205E-37739
; Sequence 37739, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37739
; LENGTH: 2992
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-37739

Query Match          91.5%; Score 572; DB 27; Length 2992;
Best Local Similarity 90.6%; Pred. No. 4.2e-58;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVSXAK 60
DB 229 EOCGAIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVLVYAK 288

QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVEGYEACMAL 117
DB 289 NNSADMIOLEKIRAPSNVSTIHIILYLPEDAKGENVQFQKODSLRVEGYEACMAL 345

RESULT 10
US-60-453-050-10999
; Sequence 10999, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10999
; LENGTH: 2992
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-10999

Query Match          91.5%; Score 572; DB 37; Length 2992;
Best Local Similarity 90.6%; Pred. No. 4.2e-58;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVSXAK 60
DB 229 EOCGAIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVLVYAK 288

QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVEGYEACMAL 117
DB 289 NNSADMIOLEKIRAPSNVSTIHIILYLPEDAKGENVQFQKODSLRVEGYEACMAL 345
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DB 289 NNSADMIOLEKIRAPSNVSTIHIILYLPEDAKGENVQFQKODSLRVEGYEACMAL 345

RESULT 11
US-60-453-135-10999
; Sequence 10999, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10999
; LENGTH: 2992
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-10999

Query Match          91.5%; Score 572; DB 37; Length 2992;
Best Local Similarity 90.6%; Pred. No. 4.2e-58;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVSXAK 60
DB 229 EOCGAIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVLVYAK 288

QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVEGYEACMAL 117
DB 289 NNSADMIOLEKIRAPSNVSTIHIILYLPEDAKGENVQFQKODSLRVEGYEACMAL 345

RESULT 12
US-60-466-412-10999
; Sequence 10999, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10999
; LENGTH: 2992
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-466-412-10999

Query Match          91.5%; Score 572; DB 37; Length 2992;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVSXAK 60
DB 229 EOCGAIMHGNNAVTFCEPYGPRELITTCNTTTASVLOFSIGSGSCRFSDPSITVLVYAK 288

QY 61 NNTADMIOLEKIRAPSNVSTVHIILYLPBEAKGESVQFQKODSLRVEGYEACMAL 117
DB 289 NNSADMIOLEKIRAPSNVSTIHIILYLPEDAKGENVQFQKODSLRVEGYEACMAL 345

RESULT 13
US-09-724-676-78128
; Sequence 78128, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
```

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; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78128
; LENGTH: 3107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-724-676-78128

Query Match          91.5%; Score 572; DB 21; Length 3107;
Best Local Similarity 90.6%; Pred. No. 4.5e-58;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNAVTFCEPYGRELTTCTANTTASVLOFSIGSGSCRFPSYSDPSITVSYAK 60
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DB 247 EOCGAIMHGNAVTFCEPYGRELTTGANTTASVLOFSIGSGSCRFPSYSDPSITVLYAK 306

QY 61 NNTADWIOLEKIRAPSVNSTVIHILYLPBEAKGESVOFQWKODSLRGEVYEACMAL 117
    |||
DB 307 NNSADWIOLEKIRAPSVNSTIHIILYLPBEAKGENVOFQWKQENLRGEVYEACMAL 363

RESULT 14
US-09-724-676A-78128
; Sequence 78128: Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78128
; LENGTH: 3107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-724-676A-78128

Query Match          91.5%; Score 572; DB 21; Length 3107;
Best Local Similarity 90.6%; Pred. No. 4.5e-58;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNAVTFCEPYGRELTTCTANTTASVLOFSIGSGSCRFPSYSDPSITVSYAK 60
    |||
DB 247 EOCGAIMHGNAVTFCEPYGRELTTGANTTASVLOFSIGSGSCRFPSYSDPSITVLYAK 306

QY 61 NNTADWIOLEKIRAPSVNSTVIHILYLPBEAKGESVOFQWKODSLRGEVYEACMAL 117
    |||
DB 307 NNSADWIOLEKIRAPSVNSTIHIILYLPBEAKGENVOFQWKQENLRGEVYEACMAL 363

RESULT 15
US-10-408-765-1624
; Sequence 1624, Application US/10408765
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
```

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; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1624
; LENGTH: 3427
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124,
; LOCATION: 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136,
; LOCATION: 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148,
; LOCATION: 149, 150, 151, 152, 153, 154, 155, 156, 157, 158
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-408-765-1624

Query Match          91.5%; Score 572; DB 30; Length 3427;
Best Local Similarity 90.6%; Pred. No. 5.1e-58;
Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EOCGTIMHGNAVTFCEPYGRELTTCTANTTASVLOFSIGSGSCRFPSYSDPSITVSYAK 60
    |||
DB 229 EOCGAIMHGNAVTFCEPYGRELTTGANTTASVLOFSIGSGSCRFPSYSDPSITVLYAK 288

QY 61 NNTADWIOLEKIRAPSVNSTVIHILYLPBEAKGESVOFQWKODSLRGEVYEACMAL 117
    |||
DB 289 NNSADWIOLEKIRAPSVNSTIHIILYLPBEAKGENVOFQWKQENLRGEVYEACMAL 345
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Search completed: August 4, 2005, 15:45:20
Job time : 495 secs

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OM protein - protein search, using sw model

Run on: August 4, 2005, 15:26:18 ; Search time 39 Seconds
(without alignments)
288.650 Million cell updates/sec

Title: US-09-897-438B-2

Perfect score: 625

Sequence: 1 EDCGRIMGNNAVTFCEPYGP.....FQWKQDSLKRGVEYEAQWAL 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	81	13.0	640	1	glucan 1,4-alpha-g
3	81	13.0	640	2	glucan 1,4-alpha-g
4	77	12.3	301	2	probable ribose me
5	74	11.8	639	2	glucan 1,4-alpha-g
6	73	11.7	639	2	glucan 1,4-alpha-g
7	72	11.5	316	2	transcription regu
8	71.5	11.4	297	2	hypothetical prote
9	70.5	11.3	868	2	conserved hypotet
10	70	11.2	1487	2	hypothetical prote
11	69.5	11.1	528	2	hypothetical prote
12	69	11.0	460	2	conserved hypotet
13	68.5	11.0	611	2	dnak-type molecula
14	68.5	11.0	977	2	seizure-related pr
15	68	10.9	249	2	hypothetical prote
16	68	10.9	304	2	galactose 1-dehydr
17	68	10.9	462	2	Cof family protein
18	68	10.9	472	2	conserved hypotet
19	68	10.9	513	2	probable protein A
20	68	10.9	816	2	hypothetical prote
21	68	10.9	818	1	peroxinectin precu
22	68	10.9	1074	2	probable En/Spm-11
23	67.5	10.8	3623	2	intrinsic factor-B
24	67	10.7	90	2	probable wound-ind
25	67	10.7	189	2	hypothetical prote
26	67	10.7	311	2	hypothetical prote
27	66.5	10.6	580	2	myo-inositol catab
28	66.5	10.6	195	2	hypothetical prote
29	66.5	10.6	1690	2	DNA-directed RNA p

30	66.5	10.6	1776	1	RRMPM	genome polypeptide
31	66	10.6	366	2	T24546	hypothetical prote
32	66	10.6	373	2	B87887	protein T05F1.5 [1
33	66	10.6	2025	2	T21588	hypothetical prote
34	65.5	10.5	377	2	F82201	spermidine/putresc
35	65.5	10.5	503	2	S36549	IL protein - human
36	65.5	10.5	540	1	A55145	chiamine-phosphate
37	65.5	10.5	549	2	T14606	probable sugar tra
38	65	10.4	112	2	T25554	hypothetical prote
39	65	10.4	359	2	H69287	hypothetical prote
40	65	10.4	417	2	H96733	hypothetical prote
41	65	10.4	422	2	A10145	probable substrate
42	65	10.4	451	2	F70743	hypothetical prote
43	65	10.4	565	1	HMIY87	hemagglutinin prec
44	65	10.4	1121	2	F86485	hypothetical prote
45	65	10.4	1187	1	A53661	protein-tyrosine-p
46	64.5	10.3	633	2	AE1344	hypothetical prote
47	64.5	10.3	747	2	T42599	minor capsid prote
48	64.5	10.3	867	1	GNLJSA	pol polypeptide -
49	64	10.2	440	2	T51278	hypothetical prote
50	64	10.2	674	2	AD3599	hemagglutinin [imp
51	64	10.2	890	2	S44150	coat protein - str
52	64	10.2	1367	1	S48478	glucan 1,4-alpha-g
53	63.5	10.2	76	2	S19773	wound-induced prot
54	63.5	10.2	126	2	E83760	hypothetical prote
55	63.5	10.2	319	2	I51569	UVS-2 protein - Af
56	63.5	10.2	406	2	G87420	amino transferase,
57	63.5	10.2	467	2	AB1379	glutamate decarbox
58	63.5	10.2	573	2	T02743	lactase (EC 1.10.3
59	63.5	10.2	753	1	WZBEE8	hypothetical prote
60	63.5	10.2	1967	2	S64604	gene 56 protein -
61	63.5	10.2	2356	2	T27790	hypothetical prote
62	63	10.1	179	2	S30994	gene 49 protein -
63	63	10.1	376	2	D40511	hypothetical prote
64	63	10.1	441	2	C87215	probable lipoprote
65	63	10.1	456	2	C97296	UDP-N-acetylglucos
66	63	10.1	817	2	D85049	probable transposo
67	63	10.1	866	2	F88481	protein C16A3.1 [1
68	63	10.1	1787	2	T21889	hypothetical prote
69	63	10.1	1805	2	T21888	hypothetical prote
70	63	10.1	4377	2	A55575	ankyrin 3, long sp
71	63	10.1	4385	2	T29042	hypothetical prote
72	62.5	10.0	149	2	T25660	hypothetical prote
73	62.5	10.0	178	2	D72281	hypothetical prote
74	62.5	10.0	190	2	A98072	conserved hypotet
75	62.5	10.0	197	2	B89843	hypothetical prote
76	62.5	10.0	467	2	AC1748	glutamate decarbox
77	62.5	10.0	506	2	AH3252	dTMP kinase (EC 2.
78	62.5	10.0	567	2	T18462	hypothetical prote
79	62.5	10.0	585	2	S48950	hypothetical prote
80	62.5	10.0	687	2	T04927	probable serine/th
81	62.5	10.0	834	2	JQ1965	hypothetical 94k p
82	62.5	10.0	867	1	GNLJMP	pol polypeptide (c
83	62.5	10.0	913	2	D90183	ATP-dependent heli
84	62	9.9	211	2	A46458	human Cbl homolog
85	62	9.9	221	2	B70844	mylodopterin bios
86	62	9.9	325	2	T04247	hypothetical prote
87	62	9.9	380	2	T05638	hypothetical prote
88	62	9.9	421	2	T40614	G beta repeat prot
89	62	9.9	448	2	S03186	Ig heavy chain C r
90	62	9.9	506	2	A86169	hypothetical prote
91	62	9.9	535	2	S56261	probable membrane
92	62	9.9	955	2	B84645	probable villin 2
93	62	9.9	1215	2	T32734	myosin-1A - Acanth
94	62	9.9	1226	2	JC7503	protein-tyrosine-P
95	62	9.9	1254	2	G86379	protein F5A9.24 [1
96	62	9.9	1337	2	T41647	probable pre-mrna
97	62	9.9	2138	2	T25810	hypothetical prote
98	61.5	9.8	176	2	S76539	hypothetical prote
99	61.5	9.8	195	2	F71164	hypothetical prote
100	61.5	9.8	335	2	T28774	hypothetical prote

ALIGNMENTS

RESULT 1
 S58870
 reelin precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2003
 C/Accession: S58870, S71844, I49297
 R/D/Accession: G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.
 Nature 374, 719-723, 1995
 A/Title: A protein related to extracellular matrix proteins deleted in the mouse mutant
 A/Reference number: I49297, MID:95211649, PMID:7715726
 A/Status: nucleic acid sequence not shown
 A/Accession: S58870
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-3461 <DAB>
 A/Cross-references: EMBL:U24703; NID:g902486; PID:g902487
 R/D/Accession: G.
 submitted to the EMBL Data Library, April 1995
 A/Reference number: S71844
 A/Accession: S71844
 A/Molecule type: mRNA
 A/Residues: 1-215 'T', 217-1905 'S', 1907-3355 'V', 3357-3391 'N', 3393-3461 <DAB>
 A/Cross-references: EMBL:U24703, NID:g902486, PID:g902487
 F/1-21/Domain: signal sequence #status predicted <SIG>
 F/28-3461/Product: reelin #status predicted <MAT>
 F/1769-1795/Domain: EGF homology <EGF>

Query Match 100.0%; Score 625; DB 2; Length 3461;
 Best Local Similarity 100.0%; Pred. No. 1.5e-56;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EOCGTIMGNAAVFCPEYGRRLTTCCLNTTASVLFQPSIGSGSCRFSSYSDPSITVSXAK 60
 DB 230 EOCGTIMGNAAVFCPEYGRRLTTCCLNTTASVLFQPSIGSGSCRFSSYSDPSITVSXAK 289

QY 61 NNTADMIOLEKTRAPSNVSTVHIILYLPBANGESVQFQMKDSLVRGEVYEACMAL 117
 DB 290 NNTADMIOLEKTRAPSNVSTVHIILYLPBANGESVQFQMKDSLVRGEVYEACMAL 346

RESULT 2
 ALASGR
 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus niger
 N/Alternate names: 1,4-alpha-D-glucan glucosylhydrolase; glucosylase
 C/Species: Aspergillus niger
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C/Accession: A30986; A91161; A05287; A22149; A25402
 R/Boel, E.; Hansen, M.T.; Hjort, I.; Hoegh, I.; Fall, N.P.
 EMBO J. 3, 1581-1585, 1984
 A/Title: Two different types of intervening sequences in the glucosylase gene from Aspe
 A/Reference number: A30986, MID:84261458, PMID:6204665
 A/Accession: A30986
 A/Molecule type: DNA
 A/Residues: 1-640 <BOB>
 A/Cross-references: UNIPROT:P04064; GB:X00712; GB:X02466; NID:92342; PIDN:CAA25303.1; PI
 A/Note: the authors translated the codon GAT for residue 317 as Asn
 R/Svensen, B.; Larsen, K.; Gunnarsson, A.
 Eur. J. Biochem. 154, 497-502, 1986
 A/Title: Characterization of a glucosylase G2 from Aspergillus niger.
 A/Reference number: A91161, MID:86136085, PMID:3081341
 A/Contents: comparison of forms G1 and G2
 A/Accession: A91161
 A/Molecule type: protein
 A/Residues: 25-640 <SVS>
 C/Comment: The large molecular form G1 is shown.
 C/Comment: Smaller molecular forms of the enzyme, G2, arise by proteolytic cleavage(s) o
 tive towards soluble poly- and oligosaccharides.
 C/Genetics:
 A/Introns: 72/1; 167/3; 200/1; 412/3
 C/Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha
 C/Keywords: alternative splicing; extracellular protein; glycoprotein; glucosidase; hyd

F/1-24/Domain: signal sequence #status predicted <SIG>
 F/23-447/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 F/25-640/Product: glucan 1,4-alpha-glucosidase G1 #status experimental <G31>
 F/25-538/Product: glucan 1,4-alpha-glucosidase G2, long form #status experimental <G32>
 F/25-536/Product: glucan 1,4-alpha-glucosidase G2, short form #status experimental <G32>
 F/195-419/Binding site: carbohydrate (asn) (covalent) #status experimental
 F/465-467,468,477,483,484,492,508,510,513,515,522,525,527,529,530,532/Binding site: carb
 F/476,486,488,496,499,500,501,502,504,506,512,514,517,518,520,524,526,528,531,534,535/Bit

Query Match 13.0%; Score 81; DB 1; Length 640;
 Best Local Similarity 25.2%; Pred. No. 2.1;
 Matches 34; Conservative 15; Mismatches 54; Indels 32; Gaps 4;

QY 9 GNAVTFCEPYGRRLTTCCLNTTASVLFQPSIGSGSCRFSSYSDPSITVSXAKN-- 61
 DB 497 GGTATTATPTGSGSVSTSKTATASKTSTSTSTCTPTTAAVATFDLTATTYGENITY 556

QY 62 -----NTADMIOLEKTRAPSNVSTVHIILYLPBANGESVQF-----Q 99
 DB 557 LVGSIQLGDMWETSDGIALSADKNTSSDPLMTYVTLTP--AGSEFYEKFIRESDDSV 613

QY 100 WKQDSLVRGEVYEAC 114
 DB 614 WESDPNREYTVQAC 628

RESULT 3
 A29166
 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus awamori
 N/Alternate names: 1,4-alpha-D-glucan glucosylhydrolase precursor; glucosylase precursor
 C/Species: Aspergillus awamori
 C/Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
 C/Accession: A29166
 R/Numbers: J.H.; Meade, J.H.; Cole, G.; Lawyer, F.C.; McCabe, P.; Schwelckart, V.; Tai, f
 Mol. Cell. Biol. 4, 2306-2315, 1984
 A/Title: Molecular cloning and characterization of the glucosylase gene of Aspergillus
 A/Reference number: A30066, MID:85085934, PMID:6440004
 A/Accession: A29166
 A/Molecule type: DNA
 A/Residues: 1-640 <NUN>
 A/Cross-references: UNIPROT:P04064; GB:X02465; NID:9454405; PIDN:AAB59296.1; PID:g166505
 C/Comment: See also PIR:ALASGR.
 C/Genetics:
 A/Introns: 72/1; 167/3; 200/1; 398/3
 C/Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha
 C/Keywords: alternative splicing; extracellular protein; glycoprotein; glucosidase; hydric
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/19-640/Product: glucan 1,4-alpha-glucosidase #status predicted <MAT>
 F/23-447/Domain: glucan 1,4-alpha-glucosidase homology <GAG>

Query Match 13.0%; Score 81; DB 2; Length 640;
 Best Local Similarity 25.2%; Pred. No. 2.1;
 Matches 34; Conservative 15; Mismatches 54; Indels 32; Gaps 4;

QY 9 GNAVTFCEPYGRRLTTCCLNTTASVLFQPSIGSGSCRFSSYSDPSITVSXAKN-- 61
 DB 497 GGTATTATPTGSGSVSTSKTATASKTSTSTSTCTPTTAAVATFDLTATTYGENITY 556

QY 62 -----NTADMIOLEKTRAPSNVSTVHIILYLPBANGESVQF-----Q 99
 DB 557 LVGSIQLGDMWETSDGIALSADKNTSSDPLMTYVTLTP--AGSEFYEKFIRESDDSV 613

QY 100 WKQDSLVRGEVYEAC 114
 DB 614 WESDPNREYTVQAC 628

RESULT 4
 T39401
 probable ribose methyltransferase - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T39401

[illegible]

A:Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallier
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtappel, S.; Hosono, S.; Hullo, M.F.;
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Parf, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Roeha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A.; Authors: Schlecht, S.; Schroeter, R.; Scoffone, F.; Seligowski, J.; Sekowska, A.; Seror,
 Kleuich, M.; Takashi, A.; Tanaka, T.; Tepstra, P.; Toononi, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunomi, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, B.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:980404033; PMID:9384377
 A:Accession: H6917
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Reads: 1-611 <KUN>
 A:Cross-references: GB:J299117; GB:AL009126; NID:g2634966; PIDN:CAB14489.1; PID:g2634993
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: dnaK
 A:Start codon: GTG
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein complex
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 11.0%; Score 68.5; DB 2; Length 611;
 Best Local Similarity 25.2%; Pred. No. 40;
 Matches 26; Conservative 20; Mismatches 40; Indels 17; Gaps 5;

QY 3 CGTTHGNAVTCPEYGPRLTTTCNTTASTAQLF-----SIGSGSCRFSPSPSTIVS 57
 DB 15 CVAVLGGG-----PVIYNAEGNRTPSVAAFRNGRGQVGVAKRQSTINPTIWS 66
 58 YAKNNTADM-IQLE-KIRAPSNVSTVI--HILYLPPEAKGESV 96
 DB 67 IKRHNGTDYKVEIEGQDYTPQEVSAIILQHLKSYASVYLGETV 109

RESULT 14
 152657
 seizure-related protein SEZ-6 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: J52657
 R:Shimizu-Nishikawa, K.; Kajiwara, K.; Kimura, M.; Katsuki, M.; Sugaya, E.
 Brain Res. Mol. Brain Res. 28, 201-210, 1995
 A:Title: Cloning and expression of SEZ-6, a brain-specific and seizure-related cDNA.
 A:Reference number: J52657; MUID:95240392; PMID:7723619
 A:Accession: J52657
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-977 <RES>
 A:Cross-references: UNIPROT:Q62269; GB:D29763; NID:g693909; PIDN:BA006167.1; PID:g693910
 F:J354-409/Domain: complement factor H repeat homology <FH01>
 F:J529-586/Domain: complement factor H repeat homology <FH02>
 F:707-762/Domain: complement factor H repeat homology <FH03>
 F:768-827/Domain: complement factor H repeat homology <FH04>
 F:835-892/Domain: complement factor H repeat homology <FH05>

Query Match 11.0%; Score 68.5; DB 2; Length 977;
 Best Local Similarity 28.3%; Pred. No. 71;
 Matches 26; Conservative 14; Mismatches 35; Indels 17; Gaps 3;

QY 19 GRELTTCLNNTTASVLFPSIGSGCRFSYSPSTIVSYAKNNTADMIOLEKIRAPSNV 78
 DB 218 GQDETTTITITITVTVQ---PRGPCSWNFSGPBG-----LDSEFLAPSSP 261
 79 STV-IHILYLPPEAKGESVQFQWKQDSLRYGE 109
 DB 262 SDVGLDCFYIVSVPGYGVIRKVENISLQEGE 293

RESULT 15

T31837
 hypothetical protein T05B4.11 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T31837
 R:Bradshaw, H.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid T05B4.
 A:Reference number: Z21092
 A:Accession: T31837
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-249

 A:Cross-references: UNIPROT:O16420; EMBL:AF016445; PIDN:AAC69060.1; GSPDB:GN00023; CESP:
 A:Experimental source: strain Bristol N2; clone T05B4
 C:Genetics:
 A:Gene: CESP.T05B4.11
 A:Map position: 5
 A:introns: 34/3; 121/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein C49G7.3

Query Match 10.9%; Score 68; DB 2; Length 249;
 Best Local Similarity 28.6%; Pred. No.15;
 Matches 22; Conservative 15; Mismatches 26; Indels 14; Gaps 4;

QY 9 GNAVTFCEPYGPRELFTT-----CLNTTASVLQFSIGSGCRPSYSDPSIT-VSYA 59
 DB 167 GNDLSICQNIQMGSFVNTYCQKSCGRCPSITTSG---YNNGGSGCTSYVADSSSNCA\$WA 223
 QY 60 KNN--TADWIQLEKIRA 74
 DB 224 KNGFCTNPFYVDQ\$RA 240

Search completed: August 4, 2005, 15:36:13
 Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2005, 15:25:38 / Search time 167 Seconds
(without alignments)
358.762 Million cell updates/sec

Title: US-09-897-438B-2

Perfect score: 625

Sequence: 1 EQCGTIMGNAVTFCEPYGP.....FMWKDSLRYGEVYEAQWAL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	1181	2	Q8C4E4
2	625	100.0	3461	1	REIN_MOUSE
3	596	95.4	3462	1	REIN_RAT
4	572	91.5	3460	1	REIN_HUMAN
5	570	91.2	216	2	Q6Q145
6	418	66.9	3209	1	REIN_CHICK
7	223	35.7	279	2	Q8C978
8	118	18.9	52	1	REIN_BOVIN
9	110.5	17.7	3008	2	Q6Q144
10	106.5	17.0	747	2	Q64FW1
11	89.5	14.3	338	2	Q93576
12	88.5	14.2	205	2	Q6PX75
13	87.5	14.0	308	2	Q8AYR0
14	87.5	14.0	635	2	Q93575
15	81	13.0	639	2	Q870C8
16	81	13.0	640	1	AMYG_ASPNG
17	80.5	12.9	291	2	Q8AY69
18	80	12.8	640	2	Q6DNH5
19	80	12.8	726	2	Q6YFE6
20	79	12.6	636	2	Q6CUT9
21	79	12.6	1078	2	Q8AKX7
22	77	12.3	301	2	Q94631
23	77	12.3	640	2	Q6DUV5
24	75	12.0	1012	2	Q6BNF2
25	75	12.0	433	2	Q8AXK6
26	74	11.8	264	2	Q64CQ4
27	74	11.8	639	1	AMYG_ASPKA
28	73.5	11.8	1130	2	Q88282
29	73	11.7	639	1	AMYG_ASPSH
30	72	11.5	316	2	Q9K569
31	72	11.5	639	2	Q12537

32	71.5	11.4	297	2	Q02128	Q02128 caenorhabdi
33	71.5	11.4	1178	2	Q7UPT4	Q7UPT4 rhodopirell
34	71	11.4	426	2	Q7MHP3	Q7MHP3 vibrio vuln
35	71	11.4	426	2	Q8DC71	Q8DC71 vibrio vuln
36	71	11.4	639	2	Q76L97	Q76L97 aspergillus
37	71	11.4	869	2	Q8BDY5	Q8BDY5 shewanella
38	71	11.4	1201	2	Q76G29	Q76G29 zea mays (m
39	70.5	11.3	221	2	Q8PIY4	Q8PIY4 streptococc
40	70.5	11.3	271	2	Q9A0X2	Q9A0X2 streptococc
41	70.5	11.3	271	2	Q8K887	Q8K887 streptococc
42	70.5	11.3	347	2	Q735K0	Q735K0 bacillus ce
43	70.5	11.3	403	2	Q8RK83	Q8RK83 mycobacteri
44	70.5	11.3	868	2	Q879X4	Q879X4 xylella fas
45	70.5	11.3	868	2	Q9PA07	Q9PA07 gorilla gor
46	70.5	11.2	123	2	Q18797	Q18797 gorilla gor
47	70	11.2	809	1	ILAR_HORSE	Q6WQ24 equus cabal
48	70	11.2	1487	2	Q8YK40	Q8YK40 anabena sp
49	69.5	11.1	125	2	Q66072	Q66072 canine hecp
50	69.5	11.1	313	2	Q88VP3	Q88VP3 lactobacill
51	69.5	11.1	528	1	VL1_HP34	Q36738 human papil
52	69.5	11.1	546	2	Q8FQX5	Q8FQX5 corynebacte
53	69.5	11.1	605	2	Q7PFC9	Q7PFC9 mus musculu
54	69.5	11.1	667	2	Q9M3P4	Q9M3P4 droseophila
55	69.5	11.1	991	2	Q7ISK2	Q7ISK2 mus musculu
56	69	11.0	364	1	DFRA_CALCH	Q759X3 asbaya goss
57	69	11.0	417	2	Q959X3	Q9K118 vibrio chol
58	69	11.0	460	2	Q9K118	Q6C777 yarrowia li
59	69	11.0	1257	2	Q6C7F3	Q6CWF5 kluyveromyc
60	68.5	11.0	210	2	Q6CWF5	Q7F592 oryza sativ
61	68.5	11.0	533	2	Q7F952	Q62224 mus musculu
62	68.5	11.0	605	2	Q62224	P17820 bacillus su
63	68.5	11.0	610	1	DNAB_BACSU	Q62269 mus musculu
64	68.5	11.0	977	2	Q62269	Q62223 mus musculu
65	68.5	11.0	991	2	Q62223	Q16420 caenorhabdi
66	68	10.9	249	2	Q16420	P11886 pseudomonas
67	68	10.9	304	1	GAL_PSEFL	Q8C014 mus musculu
68	68	10.9	383	2	Q93885	Q93885 emericeila
69	68	10.9	386	2	Q93885	Q93885 mus musculu
70	68	10.9	404	2	Q9D7F3	Q9D7F3 mus musculu
71	68	10.9	427	1	YVF5_BRAJA	P59348 bradyrhizob
72	68	10.9	448	2	Q7XRI9	Q7XRI9 oryza sativ
73	68	10.9	462	2	Q97NM3	Q97NM3 streptococc
74	68	10.9	472	2	Q8DNC5	Q8DNC5 streptococc
75	68	10.9	497	2	Q8BYL2	Q8BYL2 mus musculu
76	68	10.9	489	2	Q922P4	Q81973 arabidopsis
77	68	10.9	512	2	Q8LG73	Q9CAT3 arabidopsis
78	68	10.9	513	2	Q9CAT3	Q8BMD5 mus musculu
79	68	10.9	523	2	Q8BMD5	Q8BYN1 mus musculu
80	68	10.9	523	2	Q8BYN1	Q28331 archaeoglob
81	68	10.9	816	2	Q28331	Q26059 pacifastacu
82	68	10.9	818	2	Q26059	Q69XR6 oryza sativ
83	68	10.9	826	2	Q69XR6	Q6ZB12 oryza sativ
84	68	10.9	884	2	Q6ZB12	Q91NY8 arabidopsis
85	68	10.9	1001	2	Q91NY8	Q9C6X8 arabidopsis
86	68	10.9	1074	2	Q9C6X8	Q64BX2 sapovirus c
87	68	10.9	2281	2	Q64HX2	Q74682 aspergillus
88	67.5	10.8	427	2	Q74682	Q70Z24 rattus norv
89	67.5	10.8	3623	2	Q70Z24	Q82615 arabidopsis
90	67	10.7	90	2	Q82615	Q6C12 yarrowia li
91	67	10.7	147	2	Q6C12	Q6C12 bdellovibri
92	67	10.7	179	2	Q6M142	Q9K16 vibrio chol
93	67	10.7	189	2	Q9K16	Q73BM8 bacillus ce
94	67	10.7	236	2	Q73BM8	Q9BZ35 homo sapien
95	67	10.7	236	2	Q9BZ35	Q6NSB0 caenorhabdi
96	67	10.7	251	2	Q6NSB0	Q21182 caenorhabdi
97	67	10.7	331	2	Q21182	Q6PH48 mus musculu
98	67	10.7	497	2	Q6PH48	Q9BWJ3 homo sapien
99	67	10.7	514	2	Q9BWJ3	P42415 bacillus su
100	67	10.7	580	1	IOLD_BACSU	

ALIGNMENTS

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RESULT 1
ID Q8C4E4 PRELIMINARY; PRT; 1181 AA.
AC Q8C4E4;
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonatal cerebellum cDNA, RIKEN full-length enriched
DE library; clone: C230051M12 product: reelin, full insert sequence.
GN Name=Rein;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtractions of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnata M., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

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RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBCP databases.
CC -1 SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; AK082447; BAC38493.1; -.
DR MGD; MG1:103022; ReIn.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0004252; P:serine-type endopeptidase activity; IMP.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0016477; P:cell migration; IMP.
DR GO; GO:0009094; P:cellular morphogenesis during differentiation; IMP.
DR GO; GO:0007529; P:establishment of synaptic specificity at ne. . .; IMP.
DR GO; GO:0010001; P:glial cell differentiation; IMP.
DR GO; GO:0051057; P:positive regulation of small GTPase mediate. . .; IDA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002661; Reeler.
DR InterPro; IPR010640; Stailidase.
DR Pfam; PF02012; BNR; 4.
DR Pfam; PF02014; Reeler; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 2.
KW EGF-like domain.
SQ SEQUENCE 1181 AA; 131491 MW; 3CEA91P9EF72C720 CRC64;

Query Match 100.0%; Score 625; DB 2; Length 1181;
Best Local Similarity 100.0%; Pred. No. 3,76-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ECGTIMGNNAVTCBPYGPRLTTTCINTTASVLAQFSIGSGCRFSYSDPSITVSYAK 60
DB 230 ECGTIMGNNAVTCBPYGPRLTTTCINTTASVLAQFSIGSGCRFSYSDPSITVSYAK 289
QY 61 NNTADMIQLEKTRASNSVTHIILYLPBEAKGSEVOGKODSLRGEVYACAKL 117
DB 290 NNTADMIQLEKTRASNSVTHIILYLPBEAKGSEVOGKODSLRGEVYACAKL 346

RESULT 2
ID REIN_MOUSE STANDARD; PRT; 3461 AA.
AC Q60841; Q9CUA6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Reelin precursor (EC 3.4.21.-) (Reeler protein).
GN Name=Rein; Synonyms=RL;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Cerebellum;
RX MEDLINE=95231649; PubMed=7715726; DOI=10.1038/374719a0;
RA D'Arcangelo G., Mao G.G., Chen S.-C., Soares H.D., Morgan J.I.,
RA Curran T.;
RT "A protein related to extracellular matrix proteins deleted in the
mouse mutant reeler.";
RL Nature 374:719-723(1995).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=98086481; PubMed=9417911; DOI=10.1006/geno.1997.4983;
RA Royaux I., Lambert de Rouvroit C., D'Arcangelo G., Demitrov D.,
RA Goffinet A.M.;
RT "Genomic organization of the mouse reelin gene.";
RL Genomics 46:240-250(1997).
RN [3]
RP SEQUENCE OF 2152-3461 FROM N.A. (ISOFORM 1).
RC STRAIN=BA6B/c; TISSUE=Brain;
RX MEDLINE=95375789; PubMed=7647795;

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RA Hirotsune S., Takahara T., Sasaki N., Hirose K., Yoshiki A.,
 RA Ohashi T., Kusakabe M., Murakami Y., Muramatsu M., Watanabe S.,
 RA Nako K., Katsuki M., Hayashizaki Y.;
 RT "The reeler gene encodes a protein with an EGF-like motif expressed by
 RT pioneer neurons.";
 RT Nat. Genet. 10:77-83(1995).
 RN [4]
 RP SEQUENCE OF 3044-3461 FROM N.A. (ISOFORM 2).
 RC MEDLINE=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oseto N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.W.,
 RA Schmitt L.M., Kanpin A., Matsuda H., Batelov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brasic V., Chotina C., Corbani L.B., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada M.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmig L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirotsune-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiroaki T., Waki K., Kawai J., Aizawa K., Arkawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RT Nature 420:563-573(2002).
 RN [5]
 RP CHARACTERIZATION.
 RC MEDLINE=97141547; PubMed=8987733;
 RX D'Arcangelo G., Nakajima K., Miyata T., Ogawa M., Mikoshiba K.,
 RA Curran T.;
 RT "Reelin is a secreted glycoprotein recognized by the CR-50 monoclonal
 RT antibody.";
 RT J. Neurosci. 17:23-31(1997).
 RN [6]
 RP CHARACTERIZATION.
 RC MEDLINE=21634904; PubMed=11689558; DOI=10.1074/jbc.M106996200;
 RX Quattrocchi C.C., Wamnes F., Perisic A.M., Claret S.A.,
 RA D'Arcangelo G., Farace M.G., Keller F.;
 RT "Reelin is a serine protease of the extracellular matrix.";
 RT J. Biol. Chem. 277:303-309(2002).
 RN [7]
 RP TISSUE SPECIFICITY.
 RC MEDLINE=97325946; PubMed=9182958;
 RX Schiffmann S.N., Bernier B., Goffinet A.M.;
 RA "Reelin mRNA expression during mouse brain development.";
 RT Eur. J. Neurosci. 9:1055-1071(1997).
 RN [8]
 RP ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC MEDLINE=99263436; PubMed=10328932; DOI=10.1006/exnr.1999.7019;
 RX Lambert de Rouvroit C., Bernier B., Royaux I., de Bergeyck V.,
 RA Goffinet A.M.;
 RT "Evolutionarily conserved, alternative splicing of reelin during brain
 RT development.";
 RT Exp. Neurol. 156:229-238(1999).
 RN [9]
 RP BINDING TO VLDLR AND APOER2.
 RC MEDLINE=20036019; PubMed=10571241; DOI=10.1016/S0896-6273(00)80861-2;
 RX Hiesberger T., Trommsdorff M., Howell B.W., Goffinet A.M., Mumbly M.C.,
 RA Cooper J.A., Herz J.;

RT "Direct binding of Reelin to VLDL receptor and ApoE receptor 2 induces
 RT tyrosine phosphorylation of disabled-1 and modulates tau
 RT phosphorylation.";
 RT Neuron 24:481-489(1999).
 RN [10]
 RP FUNCTION.
 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [11]
 RP FUNCTION.
 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [12]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [13]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [14]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [15]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [16]
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 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [17]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [18]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [19]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [22]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
 RX Yip J.W., Yip Y.P.L., Nakajima K., Capricci C.;
 RT "Reelin controls position of autonomic neurons in the spinal cord.";
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [26]
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [27]
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [31]
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 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [32]
 RP FUNCTION.
 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
 RN [33]
 RP FUNCTION.
 RA MEDLINE=20359755; PubMed=10880573; DOI=10.1073/pnas.150040497;
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:8612-8616(2000).
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 RT "Reelin controls position of autonomic neurons in the spinal cord.";
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DR EMBL: D63520; BAA09788.1; AUT_INIT.
DR EMBL: AK017094; BAB30592.1; -.
DR MGD; MG1:103022; Reln.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IMP.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0016477; P:cell migration; IMP.
DR GO; GO:0000904; P:cellular morphogenesis during differentiation; IMP.
DR GO; GO:0007529; P:establishment of synaptic specificity at ne. . .; IMP.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; Glyco_hydro_BNR.
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002861; Reeler.
DR InterPro; IPR011040; Stalidase.
DR Pfam; PF02012; BNR; 15.
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DR SMART; SM00181; EGF; 5.
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DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 5.

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Query Match 100.0%; Score 625; DB 1; Length 3461;
Best Local Similarity 100.0%; Pred.No. 1.3e-57;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ECGGTIMGNATVPCPYPRRLTTTCLNTTASVLOFSIGSGCRFSYSDPSITVSXK 60
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RESULT 3
REIN RAT STANDARD; PRT; 3462 AA.
AC P58751; O80765;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Reelin precursor (EC 3.4.21.-).
GN Name=Rein;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Cerebellum;
RA Kikkawa S., Terashima T.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND DISEASE.
RC TISSUE=Cerebellum;
RX MEDLINE=22557166; PubMed=12670697; DOI=10.1016/S0169-328X(02)00650-2;
RA Yokoi N., Namee M., Wang H.-W., Kojima K., Fuse M., Yasuda K.,
RA Serikawa T., Seino S., Komeda K.;
RT "Rat neurological disease creeping is caused by a mutation in the
RT reelin gene.";
RL Brain Res. Mol. Brain Res. 112:1-7(2003).
RN [3]
RP ALTERNATIVE SPLICING.
RX MEDLINE=99263436; PubMed=10328932; DOI=10.1006/exnr.1999.7019;
RA Lambert de Rouvroit C., Bernier B., Royaux I., de Bergsyck V.,
RA Goffinet A.M.;
RT "Evolutionarily conserved, alternative splicing of reelin during brain
RT development.";
RL Exp. Neurol. 156:229-238(1999).
CC -!- FUNCTION: Extracellular matrix serine protease that plays a role

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CC in layering of neurons in the cerebral cortex and cerebellum.
CC Regulates microtubule function in neurons and neuronal migration.
CC Affects migration of sympathetic preganglionic neurons in the
CC spinal cord, where it seems to act as a barrier to neuronal
CC migration. Enzymatic activity is important for the modulation of
CC cell adhesion. Binding to the extracellular domains of lipoprotein
CC receptors VLDLR and ApoER2 induces tyrosine phosphorylation of
CC Dab1 and modulation of Tau phosphorylation (By similarity).
CC -!- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P58751-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P58751-2; Sequence=VSP_005579;
CC Name=3;
CC IsoId=P58751-3; Sequence=VSP_005580;
CC -!- TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis
CC by the Cajal-Retzius cells and other pioneer neurons located in
CC the telencephalic marginal zone and by granule cells of the
CC external granular layer of the cerebellum.
CC -!- DOMAIN: The basic C-terminal region is essential for secretion (By
CC similarity).
CC -!- DISEASE: Defects in Reelin are the cause of the creeping phenotype,
CC which is characterized by tremor, gait ataxia, cerebellar
CC hypoplasia and abnormal neuronal migration (particularly in the
CC cerebral cortex and hippocampus). The mutation is due to a
CC nucleotide insertion at codon 1892 which results in a
CC translational frameshift and truncation of the protein.
CC -!- SIMILARITY: Belongs to the reelin family.
CC -!- SIMILARITY: Contains 15 BNR repeats.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
CC -!- SIMILARITY: Contains 1 reelin domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB049473; BAB78470.1; -.
DR EMBL; AB062680; BAC75467.1; -.
DR HSSP; P05106; ILSC.
DR RGD; 3553; Reln.
DR GO; GO:0001764; P:neuronal migration; IMP.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002861; Reeler.
DR InterPro; IPR011040; Stalidase.
DR Pfam; PF02012; BNR; 15.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF02014; Reeler; 1.
DR SMART; SM00181; EGF; 6.
DR PROSITE; PS00022; EGF_1; 7.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 5.
DR PROSITE; PS51019; REELIN; 1.
KW Alternative splicing; Cell adhesion; Developmental protein;
KW EGF-like domain; Extracellular matrix; Glycoprotein; Hydrolase;
KW Repeat; Serine protease; Signal.
FT STGNAL 1 27 Potential.
FT CHAIN 28 3462 Reelin.
FT DOMAIN 28 192 Reelin.
FT DOMAIN 672 703 EGF-like 1.
FT DOMAIN 1031 1062 EGF-like 2.
FT DOMAIN 1410 1443 EGF-like 3.
FT DOMAIN 1766 1797 EGF-like 4.

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FT DOMAIN 2130 2162 EGF-like 5.
FT DOMAIN 2479 2510 EGF-like 6.
FT DOMAIN 2854 2885 EGF-like 7.
FT DOMAIN 3229 3261 EGF-like 8.
FT REPEAT 594 605 BNR 1.
FT REPEAT 800 811 BNR 2.
FT REPEAT 953 964 BNR 3.
FT REPEAT 1158 1169 BNR 4.
FT REPEAT 1324 1335 BNR 5.
FT REPEAT 1536 1547 BNR 6.
FT REPEAT 1687 1698 BNR 7.
FT REPEAT 1885 1896 BNR 8.
FT REPEAT 2044 2055 BNR 9.
FT REPEAT 2251 2262 BNR 10.
FT REPEAT 2400 2411 BNR 11.
FT REPEAT 2599 2610 BNR 12.
FT REPEAT 2779 2790 BNR 13.
FT REPEAT 2980 2991 BNR 14.
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FT CARBOHYD 291 291 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 1268 1268 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 1448 1448 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 1601 1601 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 1751 1751 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 1922 1922 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 2146 2146 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 2270 2270 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 2318 2318 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 2570 2570 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 2963 2963 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 3017 3017 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 3074 3074 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 3186 3186 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 3413 3413 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 3440 3440 N-linked (GlcNAc . . .) (Potential).
FT VARSPIC 3430 3431 Missing (in isoform 2).
FT VARSPIC 3430 3431 /Frid=VSP_005579.
FT VARSPIC 3430 3462 Missing (in isoform 3).
FT VARSPIC 3430 3462 /Frid=VSP_005580.
FT CONFLICT 336 336 H -> R (in Ref. 2).
FT CONFLICT 2714 2714 V -> L (in Ref. 2).
SQ SEQUENCE 3462 AA; 387525 MW; FCCF89B090E035F6 CRC64;

Query Match 95.4%; Score 596; DB 1; Length 3462;
Best Local Similarity 94.9%; Pred. No. 1.8e-54;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EOCCTIHGNAVTCCEPGRELTTTCANTTASVLOFSIGSGCRFSYSPSTTVSYAK 60
Db 231 EOCCTIHGNAVTCCEPGRELTTTTLNTTASVLOFSIGSGCRFSYSPSTTVSYAK 290
Qy 61 NNTADMTQLEKIRAPSNVSTVITILYLPKAGSGSVOPQWKQDSLRYGEVTEACMAL 117
Db 291 NNTADMTQLEKIRAPSNVSTVITILYLPKAGSGSVOPQWKQDSLRYGEVTEACMAL 347

RESULT 4
ID REIN_HUMAN STANDARD; PRT; 3460 AA.
AC P78509; Q86UJ0; Q86UJ8; Q8NDV0; Q9UDQ2;
DT 26-FEB-2003 (Rel. 41, Created)
DT 26-FEB-2003 (Rel. 41, Last sequence update)
DE Reelin precursor (EC 3.4.21.-).
GN Name=RELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=97202106; PubMed=9049633;
RA Desilva U., D'Arcangelo G., Braden V.V., Chen J., Miao G.G.,
RA Curran T., Green E.D.;
RT "The human reelin gene: isolation, sequencing, and mapping on
RT chromosome 7."
RL Genome Res. 7:157-164(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Rewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali U., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Coutney L., Kallio J.,
RA Ozereky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strommatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spiech J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadonoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baerach R.A., Brent M.R., Keibler E., Filcek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.B., Torrents D., Chiuwella A.T., Gish W.R.,
RA Bddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7."
RL Nature 424:157-164(2003).
RN [3]
RP ALTERNATIVE SPLICING.
RX MEDLINE=99263436; PubMed=10328932; DOI=10.1006/exnr.1999.7019;
RA Lambert de Rouvroit C., Bernier B., Royaux I., de Bergueck V.,
RA Goffinet A.M.;
RT "Evolutionarily conserved, alternative splicing of reelin during brain
RT development."
RL Exp. Neurol. 156:229-238(1999).
RN [4]
RP DISEASE, AND TISSUE SPECIFICITY.
RX MEDLINE=99080080; PubMed=9861036; DOI=10.1073/pnas.95.26.15718;
RA Impagnatello F., Guidotti A.R., Pesold C., Diwedi Y., Caruncho H.,
RA Pisu M.G., Uzunov D.P., Smalheiser N.R., Davis J.M., Pandey G.N.,
RA Pappas G.D., Tuetting P., Sharma R.P., Costa E.;
RT "A decrease of reelin expression as a putative vulnerability factor in
RT schizophrenia."
RL Proc. Natl. Acad. Sci. U.S.A. 95:15718-15723(1998).
RN [5]
RP DISEASE.
RX MEDLINE=20428190; PubMed=10973257; DOI=10.1038/79246;
RA Hong S.E., Shugart Y.Y., Huang D.T., Shanahan S.A., Grant P.E.,
RA Hourihane J.O.B., Martin N.D.T., Walsh C.A.;
RT "Autosomal recessive lissencephaly with cerebellar hypoplasia is
RT associated with human RELN mutations."
RL Nat. Genet. 26:93-96(2000).
RN [6]
RP ERATUM.
RA Hong S.E., Shugart Y.Y., Huang D.T., Shanahan S.A., Grant P.E.,
RA Hourihane J.O.B., Martin N.D.T., Walsh C.A.;
RL Nat. Genet. 27:225-225(2001).
RN [7]
RP DISEASE.
RX MEDLINE=21217116; PubMed=11317216; DOI=10.1038/mp.4000850;
RA Persico A.M., D'Aguma L., Maiorano N., Totaro A., Milferri R.,
RA Bravaccio C., Waseitnik T.H., Schneider C., Melmed R., Trillo S.,
RA Montecchi F., Palermo M., Pascucci T., Pugliesi-Allegria S.,
RA Reichelt K.-L., Conciatori M., Marino R., Quattrocchi C.C., Baldi A.,
RA Zelante L., Gasparini P., Keller F.;

```

RT "Reelin gene alleles and haplotypes as a factor predisposing to
 RT autistic disorder.";
 RL Mol. Psychiatry 6:150-159 (2001).
 CC -1- FUNCTION: Extracellular matrix serine protease that plays a role
 CC in layering of neurons in the cerebral cortex and cerebellum.
 CC Regulates microtubule function in neurons and neuronal migration.
 CC Affects migration of sympathetic preganglionic neurons in the
 CC spinal cord, where it seems to act as a barrier to neuronal
 CC migration. Enzymatic activity is important for the modulation of
 CC cell adhesion. Binding to the extracellular domains of lipoprotein
 CC receptors VLDLR and ApoER2 induces tyrosine phosphorylation of
 CC Dab1 and modulation of Tau phosphorylation (By similarity).
 CC -1- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=P78509-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P78509-2; Sequence=VSP_005575;
 CC Name=3;
 CC IsoId=P78509-3; Sequence=VSP_005576;
 CC -1- TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis
 CC by the Cajal-Retzius cells and other pioneer neurons located in
 CC the telencephalic marginal zone and by granule cells of the
 CC external granular layer of the cerebellum. In adult brain,
 CC preferentially expressed in GABAergic interneurons of prefrontal
 CC cortices, temporal cortex, hippocampus and glutamatergic granule
 CC cells of cerebellum. Also expressed in fetal and adult liver.
 CC -1- DEVELOPMENTAL STAGE: Expressed in fetal and postnatal brain and
 CC liver. Expression in postnatal human brain is high in the
 CC cerebellum.
 CC -1- DOMAIN: The basic C-terminal region is essential for secretion (By
 CC similarity).
 CC -1- DISEASE: Defects in RELN are the cause of autosomal recessive
 CC lissencephaly with cerebellar hypoplasia [MIM:257320]; also known
 CC as Norman-Roberts syndrome. Some patients also displayed
 CC persistent lymphedema neonatally, and one showed accumulation of
 CC chylous or fatty, ascites fluid.
 CC -1- DISEASE: Defects in RELN may contribute to susceptibility to
 CC schizophrenia. Expression of the protein is reduced to about 50%
 CC in patients with schizophrenia.
 CC -1- DISEASE: Defects in RELN may predispose to autistic disorder. A
 CC polymorphic GGC triplet repeat located in the 5'UTR region of RELN
 CC gene, which harbors in the normal population 8 to 10 repeats, is
 CC significantly increased in autistic patients to carry 4 to 23
 CC additional repeats.
 CC -1- SIMILARITY: Belongs to the reelin family.
 CC -1- SIMILARITY: Contains 15 BNR repeats.
 CC -1- SIMILARITY: Contains 8 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 reelin domain.
 CC -----
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 CC -----
 CC EMBL; U79716; AAC51105.1; -;
 CC EMBL; AC002067; AAM49151.1; -;
 CC EMBL; AC006981; -; NOT_ANNOTATED_CDS.
 CC EMBL; AC073208; AAP22355.1; -;
 CC EMBL; AC005101; AAP22330.1; -;
 CC EMBL; AC000121; AAB46357.2; -;
 CC EMBL; AC006316; AAD29127.1; -;
 CC EMBL; AC005064; -; NOT_ANNOTATED_CDS.
 CC HSSP; P05106; 1L5G.
 CC GeneW; HGNC:9957; RELN.
 CC MIM; 600514; -;
 CC MIM; 257320; -;

DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002860; Glyco_hydro_BNR.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002861; Reeler.
 DR InterPro; IPR011040; Stailase.
 DR Pfam; PF02012; BNR_15.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF02014; Reeler_1.
 DR SMART; SM00181; EGF_5.
 DR PROSITE; PS00022; EGF_1; 7.
 DR PROSITE; PS01186; EGF_2; 6.
 DR PROSITE; PS50026; EGF_3; 5.
 DR PROSITE; PS51019; RELN_1.
 DR PROSITE; PS51019; RELN_1.
 KW Alternative splicing; Cell adhesion; Developmental protein;
 KW EGF-like domain; Extracellular matrix; Glycoprotein; Hydrolase;
 KM Lissencephaly; Repeat; Serine protease; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 3460 Reelin.
 FT DOMAIN 26 190 Reelin.
 FT DOMAIN 670 701 EGF-like 1.
 FT DOMAIN 1029 1060 EGF-like 2.
 FT DOMAIN 1408 1441 EGF-like 3.
 FT DOMAIN 1764 1795 EGF-like 4.
 FT DOMAIN 2128 2160 EGF-like 5.
 FT DOMAIN 2477 2508 EGF-like 6.
 FT DOMAIN 2852 2883 EGF-like 7.
 FT DOMAIN 3227 3259 EGF-like 8.
 FT REPEAT 592 603 BNR 1.
 FT REPEAT 798 809 BNR 2.
 FT REPEAT 951 962 BNR 3.
 FT REPEAT 1156 1167 BNR 4.
 FT REPEAT 1322 1333 BNR 5.
 FT REPEAT 1534 1545 BNR 6.
 FT REPEAT 1685 1696 BNR 7.
 FT REPEAT 1883 1894 BNR 8.
 FT REPEAT 2042 2053 BNR 9.
 FT REPEAT 2249 2260 BNR 10.
 FT REPEAT 2398 2409 BNR 11.
 FT REPEAT 2597 2608 BNR 12.
 FT REPEAT 2777 2788 BNR 13.
 FT REPEAT 2978 2989 BNR 14.
 FT REPEAT 3362 3373 BNR 15.
 FT DOMAIN 3431 3460 Arg-rich (basic).
 Query Match 91.5%; Score 572; DB 1; Length 3460;
 Best local Similarity 90.6%; Pred. No. 6.9e-52;
 Matches 106; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ECGTIMHGNAVTFCEPYGPRELTTTCNTTASVLOFSIGSGCRFSYSDPSITYYAK 60
 DB 229 ECGAIMHGNAVTFCEPYGPRELTTTGTNTTASVLOFSIGSGCRFSYSDPSIIVLYAK 288
 QY 61 NNTAQMIOLEKTRASNVSTVTHILYLPREAGSGVOPQMKDLSRVGEVYACMAL 117
 DB 289 NNSADWIOLEKTRASNVSTIITHILYLPDAGKGVNPOKQENLKVGEVYACMAL 345
 RESULT 5
 ID 06Q145 PRELIMINARY; PRT; 216 AA.
 AC 06Q145;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DE 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 GN Reelin (Fragment).
 OS Name=RELN;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone:A730023404 product:reelin, full insert
 DE sequence.
 GN Name=Rein;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/55055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 RL [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA The FANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 RL [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multi-capillary sequencer."; Genome Res. 10:1757-1771(2000).
 RL [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurohara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tgami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahita S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK042773; BAC31362.1; -.
 DR MGI; MGI:103023; Rein.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
 DR GO; GO:0005615; C:extracellular space; IDA.

DR GO; GO:0004252; F:serine-type endopeptidase activity; IMP.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0016477; P:cell migration; IMP.
 DR GO; GO:0009094; P:cellular morphogenesis during differentiation; IMP.
 DR GO; GO:0007529; P:establishment of synaptic specificity at ne.; IMP.
 DR GO; GO:0010001; P:glial cell differentiation; IMP.
 DR GO; GO:0051057; P:positive regulation of small GTPase mediate. .; IDA.
 DR InterPro; IPR002861; Reeler.
 DR Pfam; PF02014; Reeler; 1.
 DR SEQUENCE 279 AA; 30183 MW; 267A1D24A4FABC97 CRC64;
 SQ
 Query Match 35.7%; Score 223; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.3e-15;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EOCGTIMGNNAVTFCEPYGPRELTTTCINTTASVLOFESIG 41
 DB 230 EOCGTIMGNNAVTFCEPYGPRELTTTCINTTASVLOFESIG 270
 RESULT 8
 REIN BOVIN STANDARD; PRT; 52 AA.
 ID REIN BOVIN
 AC 09n17;
 DT 28-FEB-2003 (rel. 41, Created)
 DT 28-FEB-2003 (rel. 41, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Reelin (EC 3.4.21.-) (Fragment).
 GN Name=REIN;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown Swiss;
 RA Speedel S.E., Oberg E.A., Ben Abdallah M., Denise S.K.;
 RT "Genetic analysis of candidate gene (REIN) for Weaver Syndrome in
 RT Brown Swiss cattle."; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Extracellular matrix serine protease that plays a role
 CC in layering of neurons in the cerebral cortex and cerebellum.
 CC Regulates microtubule function in neurons and neuronal migration.
 CC Affects migration of sympathetic preganglionic neurons in the
 CC spinal cord, where it seems to act as a barrier to neuronal
 CC migration. Enzymatic activity is important for the modulation of
 CC cell adhesion. Binding to the extracellular domains of lipoprotein
 CC receptors VLDLR and ApoER2 induces tyrosine phosphorylation of
 CC Dab1 and modulation of Tau phosphorylation (By similarity).
 CC -1- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis
 CC by the Cajal-Retzius cells and other pioneer neurons located in
 CC the telencephalic marginal zone and by granule cells of the
 CC external granular layer of the cerebellum.
 CC -1- SIMILARITY: Belongs to the reelin family.
 CC -----
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 CC -----
 DR EMBL; AF232904; AAF64286.1; -.
 DR Cell adhesion; Developmental protein; Hydrolase; Matrix protein;
 KW Serine protease.
 FT NON_TER 1 52 1
 FT NON_TER 52 52 1
 SQ SEQUENCE 52 AA; 6069 MW; B4699D90C998F7 CRC64;

Query Match 18.9%; Score 118; DB 1; Length 52;
Best Local Similarity 83.3%; Pred. No. 3.6e-05;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 94 ESVQPMKQDLSRNGEYEAACMAL 117
DB 1 ENVQPMKQDLSRNGEYEAACMAL 24

RESULT 9

Q6Q144 PRELIMINARY; PRT; 3008 AA.
AC Q6Q144;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Reelin (Fragment).
GN Name=RELN;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9113;
RN [1]
RP SEQUENCE FROM N.A.
RA Oberig E.A., Medrano J.F., Denise S.K.;
RU Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
DR EMBL; AY568568; AS73246.1; -.
DR InterPro; IPR006209; EGF_2.
DR InterPro; IPR006209; EGF_2.
DR InterPro; IPR006210; EGF_2.
DR InterPro; IPR011040; Sialidase.
DR Pfam; PF02012; BNR; 15.
DR Pfam; PF00008; EGF; 2.
DR SMART; SM00181; EGF; 7.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain.
FT NON TER 1
SQ SEQUENCE 3008 AA; 338763 MW; BA38AC1D9F7BA9F7 CRC64;

Query Match 17.7%; Score 110.5; DB 2; Length 3008;
Best Local Similarity 30.3%; Pred. No. 0.032;
Matches 37; Conservative 21; Mismatches 53; Indels 11; Gaps 5;

QY 3 CGTIMGNAVTFCEPYGPRELTTCLNTTASVLOF--SIGSGSCRFYSYDP-----SIT 55
DB 1023 CGTLNDGRSLYF-GKREARVPLDTRNIRLWQFTIQSGKTSGITCKIPARRNEGIV 1081

QY 56 VSYAKNNTADWIOLEKIRAPSNVTVIHILPEAKGSEVOQPMKQDLSRNGEYEAACW 115
DB 1082 VOYSDNGIIMHLRLREDFMSFLPQIISIDLPRESKTPATPRWMP--QHCK-HSAQM 1138

QY 116 AL 117
DB 1139 AL 1140

RESULT 10

Q64FW1 PRELIMINARY; PRT; 747 AA.
AC Q64FW1;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Reelin (Fragment).
GN Name=RELN;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Cerebellum;
RA Evangelisti C., Claife S.A., Maesalini S., Mannes F., Farace M.G.;
RU Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY704216; AAU14135.1; -.
FT NON TER 1
FT NON TER 747
SQ SEQUENCE 747 AA; 83810 MW; 0C196B2CF721D36 CRC64;

Query Match 17.0%; Score 106.5; DB 2; Length 747;
Best Local Similarity 30.3%; Pred. No. 0.016;
Matches 37; Conservative 20; Mismatches 54; Indels 11; Gaps 5;

QY 3 CGTIMGNAVTFCEPYGPRELTTCLNTTASVLOF--SIGSGSCRFYSYDP-----SIT 55
DB 611 CGTLNDGRSLYF-NGKREARVPLDTRNIRLWQFTIQSGKTSGITCKIPARRNEGIV 669

QY 56 VSYAKNNTADWIOLEKIRAPSNVTVIHILPEAKGSEVOQPMKQDLSRNGEYEAACW 115
DB 670 VOYSDNGIIMHLRLREDFMSFLPQIISIDLPRESKTPATPRWMP--QHCK-HSAQM 726

QY 116 AL 117
DB 727 AL 728

RESULT 11

ID 093576 PRELIMINARY; PRT; 338 AA.
AC 093576;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Reelin (Fragment).
GN Name=reln;
OS Lacerta viridis (Green lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Scincomorpha; Lacertoidae;
OC Lacertidae; Lacerta.
OX NCBI_TaxID=65476;
RN [1]
RP SEQUENCE FROM N.A.
RA Bernier B., Goffinet A.M.;
RU Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AF090951; AAC36362.1; -.
DR InterPro; IPR006209; EGF_2.
DR InterPro; IPR006210; EGF_2.
DR InterPro; IPR006210; EGF_2.
DR InterPro; IPR011040; Sialidase.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain.
FT NON TER 1
SQ SEQUENCE 338 AA; 38175 MW; C9D2142E15A388B CRC64;

Query Match 14.3%; Score 89.5; DB 2; Length 338;
Best Local Similarity 29.1%; Pred. No. 0.41;
Matches 34; Conservative 20; Mismatches 42; Indels 21; Gaps 8;

QY 3 CGTIMGNAVTFCEPYGPRELTTCLNTTASVLOF--SIGSGSCRFYSYDP-----SIT 51
DB 173 CGGLAFPAHGDLSYFNGCQ---IRQAVTKPLDTRASKIMFVQIGSLQGTDSCTNULSD 229

QY 52 P-----SITVSYAKNNTADWIOLEKIRAPSNVTVIHILPEAKGSEVOQPMKQ 102
DB 230 PNTVDAVAVLLQYSVNNGITW-QVIAQHOPDFIOAQRVSYNVLPAKMKVLLLRWQ 285

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RESULT 12
O6PX75 PRELIMINARY; PRT; 205 AA.
AC O6PX75;
DT 05-JUN-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Reelin (Fragment).
OS Crocodylus niloticus (Nile crocodile) (African crocodile).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylia; Crocodyline; Crocodylus.
OX NCBI_TaxId=8501;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2428833; PubMed=12541309; DOI=10.1002/cme.10573;
RA Tislar F., Lambert D., Rouvirot C., Sire J.Y., Meyer G., Goffinet A.M.;
RT "Reelin expression during embryonic brain development in Crocodylus
RT niloticus".
RT J. Comp. Neurol. 457:250-262 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Tislar F., Goffinet A.M.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY572417; AAS78666.1; -.
DR InterPro; IPR008976; PLAT_LH2.
FT NON_TER 1
SQ SEQUENCE 205 AA; 23709 MW; A091639964AC9A88 CRC64;

Query Match 14.2%; Score 88.5; DB 2; Length 205;
Best Local Similarity 29.1%; Pred. No. 0.29; Mismatches 42; Indels 21; Gaps 8;
Matches 34; Conservative 20;

OY 3 CGTI---MHGNAVTF--CEPYGPRELTTCLNTTASVLOF--SIGS-----GSCRFYSYD 51
DB 42 CQGLAPYAHGDSLYRNGCQ---IROAITPELDLTRASKIMFVLOIGSISQTSCTNLS 98
OY 52 P-----SITVSYAKNNTADMIQLEKIRAPSNVSVIHLILY-LPEAKGESVQFQWKQ 102
DB 99 PNTVDKAVLQYSVNNGITW-QVIAQHQPDPFIOAQRVSYNVPLBARMKGVLLRMWQ 154

RESULT 13
O8AYTO PRELIMINARY; PRT; 308 AA.
AC O8AYTO;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Reelin (Fragment).
GN Name:reln; Synonym:ReIn;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikawa S., Terashima T.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB072424; BAC20286.1; -.
DR ZFIN; ZDB-GENE-040427-1; reln1.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR008976; PLAT_LH2.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00026; EGF_3; 1.
FT NON_TER 1
SQ SEQUENCE 308 AA; 33858 MW; B2719511CC04C2F CRC64;
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Query Match 14.0%; Score 87.5; DB 2; Length 308;
Best Local Similarity 27.4%; Pred. No. 0.61;
Matches 32; Conservative 19; Mismatches 45; Indels 21; Gaps 8;

OY 3 CGTI---MHGNAVTF--CEPYGPRELTTCLNTTASVLOF--SIGS-----GSCRFYSYD 51
DB 172 CQGLAPYAHGDSLYRNGCQ---IROAVTKALDPLTRASKIMFVLOIGSVQTSCTNLDQ 228
OY 52 P-----SITVSYAKNNTADMIQLEKIRAPSNVSVIHLILY-LPEAKGESVQFQWKQ 102
DB 229 PNAVRAVLQYSVNNGSMHVIAG-HQPKDKIKAQRVSYNVPLBARMKGVLLRMWQ 284

RESULT 14
O93575 PRELIMINARY; PRT; 615 AA.
AC O93575;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Reelin (Fragment).
OS Emya orbicularis (European pond turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Emydidae; Emys.
OX NCBI_TaxId=82168;
RN [1]
RP SEQUENCE FROM N.A.
RA Bernier B., Goffinet A.M.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; AF090843; AAC35993.1; -.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR01040; Sialidase.
DR Pfam; PF02012; BNR_2.
DR Pfam; PF00008; EGF_1.
DR SMART; SM00181; EGF_2.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 615 AA; 69837 MW; A074D7AD9979C9DB CRC64;

Query Match 14.0%; Score 87.5; DB 2; Length 615;
Best Local Similarity 29.1%; Pred. No. 1.4; Mismatches 42; Indels 21; Gaps 8;
Matches 34; Conservative 20;

OY 3 CGTI---MHGNAVTF--CEPYGPRELTTCLNTTASVLOF--SIGS-----GSCRFYSYD 51
DB 450 CQGLAPYAHGDSLYRNGCQ---IROAITPELDLTRASKIMFVLOIGSISQTSCTNLS 506
OY 52 P-----SITVSYAKNNTADMIQLEKIRAPSNVSVIHLILY-LPEAKGESVQFQWKQ 102
DB 507 PNTVDKAVLQYSVNNGITW-QVIAQHQPDPFIOAQRVSYNVPLBARMKGVLLRMWQ 562

RESULT 15
O870G8 PRELIMINARY; PRT; 639 AA.
AC O870G8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Glucoamyase.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxId=5061;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=T21;
RX MEDLINE=95066018; PubMed=7975554;
RA Zhong L., Tang G., Yang K.;
RT "Isolation and sequencing of glucosylase gene from a glucosylase
RT over producing strain."
RL Wei Sheng Wu Xue Bao 34:184-190(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=T21;
RA Zhong L., Qiao D., Tang G., Yang K.;
RT "Cloning, sequencing and comparison of the 5' flanking regions of glaa
RT gene from high and low glucosylase-producing strains of *Aspergillus
RT niger*."
RL Wei Sheng Wu Xue Bao 36:181-186(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=T21;
RA Zhong L., Qiao D., Tang G., Yang K.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY250996; AAP04499.1; -.
DR HSSP; P04064; IKDM.
DR GO; GO:0003624; F:catalytic activity; IEA.
DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR GO; GO:000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR008291; Glu-a-glcad_SBD.
DR InterPro; IPR000165; Glyco_hydro_15.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00686; CBM_20; 1.
DR PIRSF; PIRSF01031; Glu-a-glcad_SBD; 1.
DR PRINTS; PR00736; GLHYDRASE15.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR PROSITE; PS001568; 68308 MM; 025AD856B542B69 CRC64;
SQ SEQUENCE 639 AA; 68308 MM; 025AD856B542B69 CRC64;

Query Match 13.0%; Score 81; DB 2; Length 639;
Best Local Similarity 25.2%; Pred. No. 7.4;
Matches 34; Conservative 15; Mismatches 54; Indels 32; Gaps 4;

QY 9 GNAVTFCEPYGPRLTTCNTTASVLPISGSGCRFSYS-----DPSITVSYAKN-- 61
DB 496 GGTATTATPTSGSVSTSKTATASKTSTSTCTPTAVAVTFDLTATTTGENTY 555
QY 62 -----NTADWIQLEKIRAPSNVSTVHILYLPKAGSVQF-----Q 99
DB 556 LVGSISQLGDMETSDGIALADKYTSSDPLMYVTLP---AGSFEYKPIRIESDDSV 612
QY 100 WKODSLRVGEVYKAC 114
DB 613 WESDPNREYTVPOAC 627

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